



```
A:Residues 13-111 <HAM>
A:Cross-references: EMBL:X54437
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-13/Domains: signal sequence (fragment) #status predicted <SIG>
F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:127-111/Domains: immunoglobulin homology <IM>
```

|                       |       |              |           |            |    |        |     |
|-----------------------|-------|--------------|-----------|------------|----|--------|-----|
| Query Match           | 78.2% | Score        | 476.5     | DB         | 2  | Length | 135 |
| Best Local Similarity | 76.3% | Pred.        | No. 1e-37 |            |    |        |     |
| Matches               | 90    | Conservative | 13        | Mismatches | 10 | Indels | 5   |
|                       |       |              |           |            |    | Gaps   | 2   |

```

Qy      2  ESGPGLVKPAQTLTSLSCAVSGGSLRSGGYWMSAIRQHPGKGLEWICYIYHSGNTYNPSSL 61
          |||||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      18  ESGPGLVKPSETLSLTCTVSGGSLRSGHYWGMIRQPPGKGLEWICSIYSGNTYNPSSL 77

```

```

Oy      62 KSRIAMSVDTSENKFSRLNSVTADTAIVYCARL--DGYTL---DIWOGTLTVVSS 114
      |||:::||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      78 KSRVTVISVDTSKNQFSLKLSSVTADTAIVYCARLGGPDYTLIDGMDVWOGTIVVSS 135

```

RESULT  
S31514

19 heavy chain - human  
 CSpecies: Homo sapiens (man)  
 CDate: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
 CAccession: S31514  
 RChastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
 submitted to the EMBL Data library, December 1992  
 A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies in Sjögren's syndrome  
 A:Reference number: S31509

A:Accession: S31514  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-128 <CBA>  
A:Cross-references: EMBL:X69862; NID:G33086; PTDN:CAA49496.1; PID:G33087  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F122-106/Domain: immunoglobulin homology <IMM>

|                       |       |              |             |            |    |        |     |
|-----------------------|-------|--------------|-------------|------------|----|--------|-----|
| Query Match           | 78.1% | Score        | 475.5       | DB         | 2  | Length | 128 |
| Best Local Similarity | 76.7% | Pred.        | No. 1.2e-37 |            |    |        |     |
| Matches               | 89    | Conservative | 10          | Mismatches | 14 | Indels | 3   |
|                       |       |              |             |            |    | Gaps   | 1   |

```
Qy      2  ESGPGLVKPAQTLSLSCAVSGGSLRGGYYWMSWIQHPPGKLEWIGIYIHSGNTYYNPDL 61
        |||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db     13  ESGPGLVRPSQTLSLTCTVSGGSLSGGFYMSWIQHPPGMALLEWHIHYFSSSTYYNPDL 72
```

```

QY      62  KSRIAMSVDTSENKFSRLINSVTADTAIVVYCARLD--GYTLDIWGQGLTVVSS  114
      |||:|||||:||||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
Db      73  KSRVITISVDTSENQFSRLITSVTPADTAIVVYCARLITNFGIGFDPMQGLTVVSS  128

```

RESULT  
S69912

Ig V-D-J region (ND) - human  
C.Species: Homo sapiens (man)  
C.Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C.Accession: S69912  
R.Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.  
Leukemia 8, 1285-1289, 1994  
A.Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multiple myeloma  
A.Reference number: S69909; MUID:9433515; PMID:8057663  
A.Accession: S69912  
A.Status: Preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA  
A:Residues: 1-122 <SAH>  
A:Cross-references: EMBL:Z33398; NID:9871347; PIDN:CAAB3849.1; PID:9887460  
A>Note: The sequence of residues 108-122 and the corresponding nucleic acid sequence are  
C:Superfamily: immunoglobulin V region, immunoglobulin homology  
P15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.48; Score 465; DB 2; Length 122;

Best Local Similarity 75.2%; Pred. No. 1.le-36;  
Matches 88; Conservative 14; Mismatches 11; Indels 4; Gaps 1.

```
QY      2 ESGPGLVKPAQTLSLSCAVSGSIRSGCYWMSMRQRHPGKGLEWICYIYHSGNTYYNPSSL 61
        |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      6 ESGPGLVKPSQTLSTLCVS GSSISSDHFMMNVRQRHPGKGLEWIGNIFYSGSSYYNPSSL 65
```

```

QY      62 KSRISAMSVDTSENKSLRLNSVTAADTA VYVCAR ---LDGYLLDIWGOGTLVTYSS 114
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      66 KSRISISVDTSKNOFSLRLKSVTAADTA VYVFCARGFFPRGTYGLDTWGOGTLVRLSS 122

```

RESULT 5  
S13519

I9 heavy chain V region precursor - human  
 CSpecies: Homo sapiens (man)  
 CDate: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 CAccession: S13519  
 R:Mottari, F.; Ochis, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
 Nucleic Acids Res. 19, 673, 1991  
 A>Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
 #Reference number: S13519; MUID:91187691; PMID:2011536

A:Accession: S13519  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-147 <MOR>  
A:Cross-references: EMBL:X56158; NID:G37724; PIDN:CAA3626.1; PID:G37725  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:41-125/Domain: immunoglobulin homology <IMV>

|                      |                 |                   |          |            |
|----------------------|-----------------|-------------------|----------|------------|
| Query Match          | 76.3%           | Score 464.5       | DB 2     | Length 147 |
| Best Local Similarly | 75.9%           | Pred. No. 1.5e-36 |          |            |
| Matches 88           | Conservative 11 | Mismatch 14       | Indels 3 | Gaps 1     |

```
OY      2   ESGPGLVKPAQTLTSLSCAVSSGGSIRSGGYWMSWIRQHPGKLEWIGIYIHSGNTYYNPSSL 61
          |||||::||||:|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      32   ESGPGLVKPSELTSLCTVSSGGSISSSSITYMGWRQPCKGLEWIGSITYSGSTYYNPSSL 9
```

| QY                                     | Db  |
|--|---|
| 62                                     | 92  |
| KSRIANSVDTSSENKFSLRLSNVAADTA VYVCAR--- | KSRIANSVDTSKNOFSLKLSNVAADTA VYVCARDLMPFGLFDYWGOGTLVTVSS |
| LDGYTLDIWGOGTLVTVSS                    | 147   |

RESULT 6  
S30534

Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Jan-1995 #sequence  
 C:Accession: S30534  
 R:Mariette, X.  
 submitted to the EMBL Data Library, October.1992

A;Accession: S30534  
A;Status: preliminary  
A;Molecule type: mRNA

A:Residues: 1-130 <MAR>  
A:Cross-references: EMBL:Z18320  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:15-99/Domain: immunoglobulin homology <IMM>

|                          |        |                    |            |             |
|--------------------------|--------|--------------------|------------|-------------|
| Query Match              | 75.5%; | Score 460;         | DB 2;      | Length 130; |
| Best Local Similarity    | 72.8%; | Pred. No. 3.5e-36; |            |             |
| Matches 91; Conservative | 10;    | Mismatches 12;     | Indels 12; | Gaps 2      |

**OY**

2 ESGPGLVKPAQTLTSLSCAVSSGGSIRSGGYWMSWRQHPPKGLEWIGIYIHSGNTYYNPSL 6  
||||| : ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||  
6 ESGPGLVKPSQTLSLTCTVSSGGSISGGSYWMSWRQPAGKGLEWIGRIYTSGSTNNPSL 6

**Db**

```

62 KSRTAMSVDTSNFKSLRLNSVTADTAVVYCARLDG-----YT-----LDIWGGTL 109
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db 66 KSRVTISVPTSKNPFLKLSVTAADTAVYYCARDKGGFWMGYITRNSRAADIWGGITM 125

```

Oy 110 VTSS 114  
 |||||  
 Db 126 VTSS 130

## RESULT 7

137782  
 Ig variable region (VDJ) (clone T23-9) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
 C:Accession: J37782; S25476  
 R:Demaison, C.; Chastagner, P.; There, J.; Zouali, M.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
 A:Title: Somatic diversification in the heavy chain variable region genes expressed by h  
 A:Reference number: A36876; MUID:9411917; PMID:8290556  
 A:Accession: J37782  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-140 <RES>  
 A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 458.5; DB 2; Length 140;  
 Best Local Similarity 75.4%; Pred. No. 5.2e-36;  
 Matches 89; Conservative 12; Mismatches 10; Indels 7; Gaps 2;

Oy 2 ESGPLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPBL 61  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 25 ESGPLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPBL 82  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Oy 62 KSRIAMSVDTSENKFSRLNVTADTAVYVCARDL-----GYTDINGGCTLVTVSS 114  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 83 KSRVTLSDVTSKQPSLKLSSVTADTAVYVCARNSSWYGRYEDYWGQGLTVTVSS 140  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

## RESULT 8

S26801  
 Ig heavy chain V region (DP-65) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 13-Jan-1995 #sequence\_revision 25-Oct-1996 #text\_change 20-Jun-2000  
 C:Accession: S26801; S26900  
 R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
 Eur. J. Immunol. 22, 1075-1082, 1992  
 A:Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.  
 A:Reference number: S26800; MUID:92201299; PMID:1348029  
 A:Accession: S26801  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-99 <MEN>  
 A:Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g1335372  
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 776-798, 1992  
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
 A:Reference number: S26885; MUID:93021117; PMID:1404388  
 A:Accession: S26900  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-99 <TOM>  
 A:Cross-references: EMBL:Z12365; NID:g32948; PIDN:CAA78235.1; PID:g32949  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 453; DB 2; Length 99;  
 Best Local Similarity 86.2%; Pred. No. 1.2e-35;  
 Matches 81; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ESGPLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPBL 61  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 6 ESGPLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPBL 65  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 62 KSRIAMSVDTSENKFSRLNVTADTAVYVCAR 95  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 66 KSRVTLSDVTSKQPSLKLSSVTADTAVYVCAR 99  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

## RESULT 9

S09710  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S09710  
 R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
 Biochem. J. 268, 135-140, 1990  
 A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains o  
 A:Reference number: S09710; MUID:90262535; PMID:2111699  
 A:Accession: S09710  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-146 <HUG>  
 A:Cross-references: GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g31448  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 452.5; DB 2; Length 146;  
 Best Local Similarity 68.3%; Pred. No. 2e-35;  
 Matches 84; Conservative 16; Mismatches 12; Indels 11; Gaps 2;

Oy 2 ESGPLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPBL 61  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 25 ESGPLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPBL 84  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Oy 62 KSRIAMSVDTSENKFSRLNVTADTAVYVCARDL-----TLIDINGGCTLVTV 111  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 85 KSRVTLSDVTSKQPSLKLSSVTADTAVYVCARLPGYGDTSVRKRVNMDLWGQGLTVT 143  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 112 VSS 114  
 |||||  
 Db 144 VSS 146

## RESULT 10

S44113  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
 C:Accession: S44113  
 R:Hawkins, R.E.; Zhu, D.; Orecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
 submitted to the EMBL Data Library, March 1994  
 A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r  
 A:Reference number: S44105  
 A:Accession: S44113  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-121 <HAM>  
 A:Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA33264.1; PID:g940524  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 451.5; DB 2; Length 121;  
 Best Local Similarity 73.3%; Pred. No. 2e-35;  
 Matches 85; Conservative 13; Mismatches 15; Indels 3; Gaps 2;

Oy 2 ESGPLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPBL 61  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 6 ESGPLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPBL 65  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Oy 62 KSRIAMSVDTSENKFSRLNVTADTAVYVCARDL--YT-LDINGGCTLVTVSS 114  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 66 KSRVTLSDVTSKQPSLKLSSVTADTAVYVCARLPGYGDTSVRKRVNMDLWGQGLTVT 121  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||







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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 : Search time 6.39091 Seconds  
(without alignments)  
838.855 Million cell updates/sec

Title: US-10-027-725A-7

Sequence: 1 ESEGLVKAQTLSLSCAV.....RLDGYTLIDMGQGLVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 419.5 | 68.9        | 129    | 1 HV2F_HUMAN | P01824 homo sapien |
| 2          | 405   | 66.5        | 126    | 1 HV2I_HUMAN | P06331 homo sapien |
| 3          | 374.5 | 61.5        | 137    | 1 HV46_MOUSE | P01822 mus musculu |
| 4          | 369.5 | 60.7        | 117    | 1 HV2G_HUMAN | P01825 homo sapien |
| 5          | 361.5 | 59.4        | 113    | 1 HV47_MOUSE | P01823 mus musculu |
| 6          | 342.5 | 56.2        | 116    | 1 HV61_MOUSE | P18532 mus musculu |
| 7          | 341.5 | 56.1        | 116    | 1 HV60_MOUSE | P18531 mus musculu |
| 8          | 334   | 54.8        | 117    | 1 HV62_MOUSE | P18533 mus musculu |
| 9          | 321.5 | 52.8        | 144    | 1 HV43_MOUSE | P01819 mus musculu |
| 10         | 304   | 49.9        | 135    | 1 HV02_XENLA | P20957 xenopus lae |
| 11         | 300   | 49.3        | 120    | 1 HV2B_HUMAN | P01815 homo sapien |
| 12         | 295   | 48.4        | 119    | 1 HV40_MOUSE | P01810 mus musculu |
| 13         | 293   | 48.1        | 122    | 1 HV3A_HUMAN | P01762 homo sapien |
| 14         | 288   | 47.3        | 119    | 1 HV38_MOUSE | P01808 mus musculu |
| 15         | 285.5 | 46.9        | 119    | 1 HV2C_HUMAN | P01816 homo sapien |
| 16         | 285   | 46.8        | 119    | 1 HV37_MOUSE | P01807 mus musculu |
| 17         | 282.5 | 46.4        | 121    | 1 HV3J_HUMAN | P01771 homo sapien |
| 18         | 280.5 | 46.1        | 117    | 1 HV2B_RABIT | P01828 oryctolagus |
| 19         | 278.5 | 45.7        | 125    | 1 HV2D_HUMAN | P01817 homo sapien |
| 20         | 276   | 45.3        | 114    | 1 HV3B_HUMAN | P01763 homo sapien |
| 21         | 275   | 45.2        | 122    | 1 HV3E_HUMAN | P01768 homo sapien |
| 22         | 274.5 | 45.1        | 121    | 1 HV2E_HUMAN | P01818 homo sapien |
| 23         | 274   | 45.0        | 116    | 1 HV05_CARAU | P19181 carassius a |
| 24         | 273   | 44.8        | 122    | 1 HV3H_HUMAN | P01769 homo sapien |
| 25         | 272   | 44.7        | 114    | 1 HV2A_RABIT | P01827 oryctolagus |
| 26         | 272   | 44.7        | 122    | 1 HV2I_MOUSE | P01790 mus musculu |
| 27         | 271   | 44.5        | 147    | 1 HV2H_HUMAN | P01767 homo sapien |
| 28         | 270.5 | 44.4        | 115    | 1 HV3F_HUMAN | P01767 homo sapien |
| 29         | 270.5 | 44.4        | 117    | 1 HV4I_MOUSE | P01811 mus musculu |
| 30         | 270   | 44.3        | 115    | 1 HV44_MOUSE | P01820 mus musculu |
| 31         | 270   | 44.3        | 122    | 1 HV20_MOUSE | P01789 mus musculu |
| 32         | 269.5 | 44.3        | 142    | 1 HV01_RAT   | P01805 rattus norv |
| 33         | 268.5 | 44.1        | 115    | 1 HV3D_HUMAN | P01765 homo sapien |

|    |       |      |     |              |                    |
|----|-------|------|-----|--------------|--------------------|
| 34 | 268.5 | 44.1 | 117 | 1 HV42_MOUSE | P01812 mus musculu |
| 35 | 267.5 | 43.9 | 117 | 1 HV12_MOUSE | P01756 mus musculu |
| 36 | 267.5 | 43.9 | 123 | 1 HV25_MOUSE | P01794 mus musculu |
| 37 | 267   | 43.8 | 116 | 1 HV45_MOUSE | P01821 mus musculu |
| 38 | 267   | 43.8 | 126 | 1 HV2A_HUMAN | P01814 homo sapien |
| 39 | 267   | 43.8 | 139 | 1 HV07_MOUSE | P01751 mus musculu |
| 40 | 266.5 | 43.8 | 117 | 1 HV13_MOUSE | P01757 mus musculu |
| 41 | 266.5 | 43.8 | 118 | 1 HV39_MOUSE | P01809 mus musculu |
| 42 | 266.5 | 43.8 | 123 | 1 HV22_MOUSE | P01791 mus musculu |
| 43 | 265.5 | 43.6 | 123 | 1 HV18_MOUSE | P01787 mus musculu |
| 44 | 265.5 | 43.6 | 123 | 1 HV19_MOUSE | P01788 mus musculu |
| 45 | 264.5 | 43.4 | 123 | 1 HV24_MOUSE | P01793 mus musculu |

## ALIGNMENTS

## RESULT 1

ID HV2F\_HUMAN STANDARD; PRT; 129 AA.

AC P01824, 1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region WAH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]

RP MEDLINE=8222235; PubMed=6806818;

RA Takahashi N., Tetaert D., Debure B., Lin L.-C., Putnam F.W.;  
RT "Complete amino acid sequence of the delta heavy chain of human  
immunoglobulin D.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).

CC -! MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA  
PROTEIN

CC -! SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR: A02099; D2HWA.

DR HSSP; P01825; 7FAB.

DR GLYcositedB; P01824; -.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:Immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV\_1.

DR PROSITE; PS50835; IG-LIKE; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 113 IG-LIKE.

FT NON TER 129 129

SQ SEQUENCE 129 AA; 14117 MW; D5D5D47ABE51319 CRC64;

Query Match 68.9%; Score 419.5; DB 1; Length 129;  
Best local similarity 62.7%; Pred. No. 3.5e-38;  
Matches 79; Conservative 16; Mismatches 16; Indels 15; Gaps 2;

|    |     |   |     |
|----|-----|---|-----|
| QY | 2   | ESGGLVKAQTLSLSCAVSGSIRSGGYSWIRQHPGKLEWIGVYHSGNRYNSL   | 61  |
| DB | 6   | ESGGLVKAQTLSLSCAVSGSIRSGGYSWIRQHPGKLEWIGVYHSGNRYNSL   | 65  |
| QY | 62  | KSRIAMVDISENFSEKSLNSVTADTAIVVYCAR-----LDGYTLIDMGQGT   | 108 |
| DB | 66  | RGRTISVDISRNQPSLIRMSAADTAMYYCAGNPPYDIGNGSDG--IDVWGQGT | 123 |
| QY | 109 | LVTYSS 114  |     |
| DB | 124 | TVHVS 129   |     |

RESULT 2  
 HVT1\_HUMAN  
 ID HV21\_HUMAN STANDARD; PRT; 146 AA.  
 AC P06331;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-II region ARH-77 precursor.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RX MEDLINE=85205332; PubMed=3922855;  
 RA Kudo A., Ishihara T., Nishimura Y., Matanabe T.;  
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-  
 RT repeat sequence in 5' flanking region.";  
 RL Gene 33:181-189 (1985).  
 DR PIR: A02101; GIMH2.  
 DR HSSP: P01825; 7PAB.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IG\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.  
 FT DOMAIN 20 117 V SEGMENT.  
 FT DOMAIN 118 127 D SEGMENT.  
 FT DOMAIN 128 146 J SEGMENT.  
 FT DISULFID 42 115 BY SIMILARITY.  
 FT NON\_TER 146 146  
 SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 66.5%; Score 405; DB 1; Length 146;  
 Best Local Similarity 66.9%; Pred. No. 1,4e-36;  
 Matches 81; Conservative 13; Mismatches 15; Indels 12; Gaps 3;

QY 4 GPGLVPAQTLSGCAVSGSGSYGYSWIRQPKGLEWYGYTHSGNTYNSLKS 63  
 DB 28 GAGLVPRSELTSLTCVFGGSF--SGYWMIRQPKGLEWYGYTHSGNTYNSLKS 85  
 QY 64 RIMASVDTSENKPSLRNSTVTAADTAVYYCAR--LDG-----YTLDIWGQGLVTVS 113  
 DB 86 RVTISLDTSKNLSLKLSTVTAADTAVYYCARGLRGGANDVDVYIGMDVGGQITVTVS 145  
 QY 114 S 114  
 DB 146 S 146

RESULT 3  
 HVA6\_MOUSE  
 ID HVA6\_MOUSE STANDARD; PRT; 137 AA.  
 AC P01852;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig heavy chain V region MOPC 315 precursor.  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX MEDLINE=89238351; PubMed=2497341;  
 RA Rinfret A., Horne C., Dorrington K.J., Klein M.

RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH  
 RT gene segment.";  
 RL Mol. Immunol. 26:431-434 (1989).  
 RN (2)  
 RN SEQUENCE OF 1-31.  
 RX MEDLINE=78094475; PubMed=414225;  
 RA Jilka R.L., Peetka S.;  
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse  
 RT immunoglobulin heavy chain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).  
 RN (3)  
 RN SEQUENCE OF 1-21.  
 RX MEDLINE=79148758; PubMed=428562;  
 RA Schechter I., Wolf O., Zemell R., Burestein Y.;  
 RT "Structure and function of immunoglobulin genes and precursors.";  
 RL Fed. Proc. 38:1835-1845 (1979).  
 RN (4)  
 RN SEQUENCE OF 19-136.  
 RX MEDLINE=74170779; PubMed=4524622;  
 RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;  
 RT "Amino-acid sequence of the variable region of the heavy (alpha)  
 RT chain of a mouse myeloma protein with anti-hapten activity.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).  
 RN (5)  
 RN REVISION TO 53.  
 RX MEDLINE=77244979; PubMed=268248;  
 RA Hood L., Margolies M.N., Givol D., Zakut R.;  
 RL Unpublished results, cited by:  
 RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;  
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).  
 CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA  
 CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M27638; AAA61337.1; -  
 CC EMBL: X07880; CAA30727.1; -  
 CC PIR: P10102; AVMS35.  
 DR HSSP: P01825; 7PAB.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IGV\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.  
 FT DOMAIN 19 48 FRAMEWORK-1.  
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 84 FRAMEWORK-3.  
 FT DOMAIN 85 116 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 117 126 FRAMEWORK-4.  
 FT DOMAIN 127 137 BY SIMILARITY.  
 FT DISULFID 40 114  
 FT CONFLICT 15 15 G->G (IN REF. 1; CAA30727).  
 FT CONFLICT 15 15 G->H (IN REF. 2).  
 FT CONFLICT 77 78 GY->YG (IN REF. 4).  
 FT CONFLICT 102 102 N->D (IN REF. 4).  
 FT CONFLICT 123 123 MISSING (IN REF. 4).  
 FT NON\_TER 137 137  
 SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 61.5%; Score 374.5; DB 1; Length 137;  
 Best Local Similarity 61.7%; Pred. No. 2.6e-33;  
 Matches 71; Conservative 20; Mismatches 21; Indels 3; Gaps 2;

OY 2 ESGGVLVPAQTSLSCAVSGGSIIRSGGYWMTIRHGPGLKLEWIGYIYHSGNTYVPSL 61  
 DB 24 ESGGVLVPSQSLSITCSVTYSITS-GYFNNWIRPFGNKLKLEWIGYIYHSGNTYVPSL 82  
 OY 62 KSRIAMSVDTSENKFSRLNSVTADTAVVYCARLDG--YTLIDWGGTTLTVSS 114  
 DB 83 KNRISITRDTSENQFPLKLNSTVEDTATYTCAGNDHLVYFDYWGQGTTLTVSS 137

RESULT 4  
 HV2G HUMAN STANDARD; PRT; 117 AA.  
 AC P01825;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region NEMM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77242302; PubMed=407927;  
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;  
 RT "Amino acid sequence of the VH region of a human myeloma  
 RT Immunoglobulin (IgG New).";  
 RL Biochemistry 16:3412-3420(1977).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.  
 RX MEDLINE=78066916; PubMed=618887;  
 RA Saul P.A., Anzel L.W., Poljak R.J.;  
 RT "Preliminary refinement and structural analysis of the Fab fragment  
 RT from human immunoglobulin new at 2.0-A resolution.";  
 RL J. Biol. Chem. 253:585-597(1978).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 CC PROTEIN.  
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC PIR; A90404; G1HNM.  
 DR PDB; 7FAB; 31-JAN-94.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 111  
 FT MOD\_RES 1 1  
 FT STRAND 3 7  
 FT TURN 11 12  
 FT TURN 14 15  
 FT STRAND 18 25  
 FT TURN 30 31  
 FT STRAND 33 39  
 FT TURN 41 42  
 FT STRAND 46 51  
 FT TURN 53 54  
 FT STRAND 57 59  
 FT HELIX 61 63  
 FT TURN 64 66  
 FT STRAND 67 72  
 FT TURN 73 76  
 FT STRAND 77 82  
 FT HELIX 87 89  
 FT STRAND 91 98  
 FT STRAND 104 107  
 FT STRAND 111 115  
 FT NON\_TER 117 117

SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;  
 Query Match 60.7%; Score 369.5; DB 1; Length 117;  
 Best Local Similarity 61.4%; Pred. No. 7,4e-33;  
 Matches 70; Conservative 22; Mismatches 19; Indels 3; Gaps 2;

OY 2 ESGGVLVPAQTSLSCAVSGGSIIRSGGYWMTIRHGPGLKLEWIGYIYHSGNTYVPSL 61  
 DB 6 ESGGVLVPSQSLSITCSVTYSITS--YNNWIRKPKNKLKLEWIGYIYHSGNTYVPSL 63

OY 62 KSRIAMSVDTSENKFSRLNSVTADTAVVYCARLDG--YTLIDWGGTTLTVSS 114  
 DB 64 KSRVITLVDTSENQFSLRLNSVTADTAVVYCARLDG--YTLIDWGGTTLTVSS 117

RESULT 5  
 HV47 MOUSE STANDARD; PRT; 113 AA.  
 AC P01823;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 36-60.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=84024551; PubMed=6414509;  
 RA Juszczak E.C., Margolies M.N.;  
 RT "Amino acid sequence of the heavy chain variable region from the A/J  
 RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor  
 RT idioType.";  
 RL Biochemistry 22:4291-4296(1983).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTARSONATE  
 CC MONOCLONAL ANTIBODY OF THE ICG2A SUBCLASS. IT REPRESENTS A SECOND  
 CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTARSONATE RESPONSE OF  
 CC STRAIN A/J MICE.  
 CC PIR; A02098; G2MS60.  
 DR PDB; 1J10; 18-FEB-03.  
 DR PDB; 1J1P; 18-FEB-03.  
 DR PDB; 1J1X; 18-FEB-03.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; 3D-structure.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12734 MW; 38DC0E3F5075B7 CRC64;

Query Match 59.4%; Score 361.5; DB 1; Length 113;  
 Best Local Similarity 62.8%; Pred. No. 5,1e-32;  
 Matches 71; Conservative 18; Mismatches 19; Indels 5; Gaps 2;

OY 2 ESGGVLVPAQTSLSCAVSGGSIIRSGGYWMTIRHGPGLKLEWIGYIYHSGNTYVPSL 61  
 DB 6 ESGGVLVPSQSLSITCSVTYSITS--YNNWIRKPKNKLKLEWIGYIYHSGNTYVPSL 63

OY 62 KSRIAMSVDTSENKFSRLNSVTADTAVVYCARLDG--YTLIDWGGTTLTVSS 114  
 DB 64 KSRISITRDTSENQFPLKLNSTVEDTATYTCAGNDHLVYFDYWGQGTTLTVSS 117

RESULT 6  
 HV61 MOUSE STANDARD; PRT; 116 AA.  
 AC P18532;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 1B43 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=BALB/CJ;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 the primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC 1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.  
 DR PIR; JT0508; HWSJ1B.  
 DR PDB; 1KCS; 11-MAY-02.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; Signal; 3D-structure.  
 FT SIGNAL 1 18  
 FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.  
 FT DOMAIN 19 48 FRAMEWORK-1.  
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 54 67 FRAMEWORK-2.  
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 85 116 FRAMEWORK-3.  
 FT DISULFID 40 114 BY SIMILARITY.  
 FT NON TER 116 116  
 SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681F74 CRC64;  
 Query Match 56.2%; Score 342.5; DB 1; Length 116;  
 Best Local Similarity 69.1%; Pred. No. 5.9e-30;  
 Matches 65; Conservative 13; Mismatches 15; Indels 1; Gaps 1;  
 QY 2 ESGPGLVKPAQTLISLCANVSGSIRSGGYWMSIRHPGKLEWIGIYHSGNTYYPSTL 61  
 DB 24 ESGPDLVKPSQSLSTCTVYGSITS-GYSWMHIRQPKMKLEWIGIYHSGNTYYPSTL 82  
 QY 62 KSRIMSVDTSENKFSRLNSTVADTAATVYCAR 95  
 DB 83 KSRISITRDTSKNQFPLQINSVTTEDTATVYCAR 116  
 RESULT 7  
 HV60 MOUSE STANDARD; PRT; 116 AA.  
 ID HV60\_MOUSE  
 AC P18531;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-UTL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region M315 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=BALB/CJ;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 the primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 DR PIR; JT0509; HWSJ1.  
 DR HSSP; P01825; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.  
 FT DOMAIN 19 53  
 FT DOMAIN 54 67 FRAMEWORK-1.  
 FT DOMAIN 68 84 FRAMEWORK-2.  
 FT DOMAIN 85 116 COMPLEMENTARITY-DETERMINING-2.  
 FT DISULFID 40 114 BY SIMILARITY.  
 FT NON TER 117 117  
 SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;  
 Query Match 54.8%; Score 334; DB 1; Length 117;  
 Best Local Similarity 64.9%; Pred. No. 4.9e-29;  
 Matches 61; Conservative 14; Mismatches 19; Indels 0; Gaps 0;  
 QY 2 ESGPGLVKPAQTLISLCANVSGSIRSGGYWMSIRHPGKLEWIGIYHSGNTYYPSTL 61  
 DB 24 ESGPDLVKPSQSLSTCTVYGSITS-GYSWMHIRQPKMKLEWIGIYHSGNTYYPSTL 82

DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.  
 FT DOMAIN 19 48 FRAMEWORK-1.  
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 54 67 FRAMEWORK-2.  
 FT DOMAIN 68 84 FRAMEWORK-3.  
 FT DOMAIN 85 116 COMPLEMENTARITY-DETERMINING-2.  
 FT DISULFID 40 114 BY SIMILARITY.  
 FT NON TER 116 116  
 SQ SEQUENCE 116 AA; 13095 MW; 4562E03E5D3C9E10 CRC64;  
 Query Match 56.1%; Score 341.5; DB 1; Length 116;  
 Best Local Similarity 67.0%; Pred. No. 7.5e-30;  
 Matches 63; Conservative 16; Mismatches 14; Indels 1; Gaps 1;  
 QY 2 ESGPGLVKPAQTLISLCANVSGSIRSGGYWMSIRHPGKLEWIGIYHSGNTYYPSTL 61  
 DB 24 ESGPDLVKPSQSLSTCTVYGSITS-GYSWMHIRQPKMKLEWIGIYHSGNTYYPSTL 82  
 QY 62 KSRIMSVDTSENKFSRLNSTVADTAATVYCAR 95  
 DB 83 KSRISITRDTSKNQFPLQINSVTTEDTATVYCAR 116  
 RESULT 8  
 HV62 MOUSE STANDARD; PRT; 117 AA.  
 ID HV62\_MOUSE  
 AC P18533;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 733 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=BALB/CJ;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 the primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; JT0510; HWSJ73.  
 DR HSSP; P01825; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.  
 FT DOMAIN 19 53  
 FT DOMAIN 54 67 FRAMEWORK-1.  
 FT DOMAIN 68 84 FRAMEWORK-2.  
 FT DOMAIN 85 116 COMPLEMENTARITY-DETERMINING-2.  
 FT DISULFID 40 115 BY SIMILARITY.  
 FT NON TER 117 117  
 SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;  
 Query Match 54.8%; Score 334; DB 1; Length 117;  
 Best Local Similarity 64.9%; Pred. No. 4.9e-29;  
 Matches 61; Conservative 14; Mismatches 19; Indels 0; Gaps 0;  
 QY 2 ESGPGLVKPAQTLISLCANVSGSIRSGGYWMSIRHPGKLEWIGIYHSGNTYYPSTL 61  
 DB 24 ESGPDLVKPSQSLSTCTVYGSITS-GYSWMHIRQPKMKLEWIGIYHSGNTYYPSTL 82

QY 62 KSRIAMSVDTSENFSLRSLNSVTADTAVYYCAR 95  
 DB 84 KSRITTRDTKNOFPLENNSLTADTAVYYCAR 117

RESULT 9  
 HY43\_MOUSE  
 ID HY43\_MOUSE STANDARD; PRT; 144 AA.

AC P01819;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region MOPC 141 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

SEQUENCE FROM N.A.  
 RX MEDLINE=81012133; PubMed=6774258;  
 RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;  
 RT "Two types of somatic recombination are necessary for the generation  
 of complete immunoglobulin heavy-chain genes.";  
 RL Nature 286:676-683(1980).  
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A  
 CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 CC -----

DR EMBL; V00768; CA24149.1; -  
 DR PIR; A02094; G2MS14.  
 DR HSSP; P01825; 7FAB.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.  
 FT DOMAIN 20 130 IG-LIKE.  
 FT NON\_TER 144 144  
 FT SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match  
 Best Local Similarity 52.8%; Score 321.5; DB 1; Length 144;  
 Matches 66; Conservative 21; Mismatches 24; Indels 11; Gaps 3;

QY 2 ESGPGLVPAQTLTSLSCAVSGSIRSGGYMSWRHQPCKGLEWIGYIHSGNTYVPSL 61  
 DB 25 ESGPGLVPAQSLSTICTYSGFSLT--GYGVNVMVQPPKGLGEMIGTIMGNSTYVPSL 82

QY 62 KSRIAMSVDTSENFSLRSLNSVTADTAVYYCAR-----RLDGY-TLTDWGQGLTVV 112  
 DB 83 KSRITTRDTKNOFPLENNSLTADTAVYYCAR-----RLDGY-TLTDWGQGLTVV 142

QY 113 SS 114  
 DB 143 SS 144

RESULT 10  
 HY02\_XENLA  
 ID HY02\_XENLA STANDARD; PRT; 135 AA.

AC P20957;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region XIG14 precursor (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8335;  
 RN [1]

SEQUENCE FROM N.A.  
 RX MEDLINE=88176921; PubMed=2451244;  
 RA Schwager J., Mikoryak C.A., Steiner L.A.;  
 RT "Amino acid sequence of heavy chain for evolution of immunoglobulin  
 from cDNA sequence: implications for evolution of immunoglobulin  
 domains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 CC -----

DR EMBL; J03632; AAA9791.1; -  
 DR PIR; B31933; B31933.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL 1 18  
 FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.  
 FT DOMAIN 20 128 IG-LIKE.  
 FT NON\_TER 135 135  
 FT SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match  
 Best Local Similarity 49.9%; Score 304; DB 1; Length 135;  
 Matches 59; Conservative 19; Mismatches 33; Indels 4; Gaps 2;

QY 2 ESGPGLVPAQTLTSLSCAVSGSIRSGGYMSWRHQPCKGLEWIGYIHSGNTYVPSL 61  
 DB 23 ESGPGLVPAQSLSTICTYSGFSLT--YHNMWRHQPCKGLEWIGYIATGSTRADSL 80

QY 62 KSRIAMSVDTSENFSLRSLNSVTADTAVYYCAR--LDGYTLTDWGQGLTVVSS 114  
 DB 81 KSRITTRDTKNOFPLENNSLTADTAVYYCAR-----RLDGY-TLTDWGQGLTVVSS 135

RESULT 11  
 HY2B\_HUMAN  
 ID HY2B\_HUMAN STANDARD; PRT; 120 AA.

AC P01815;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region COR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

SEQUENCE  
 RX MEDLINE=70258837; PubMed=5449120;

RA Press E.M., Hogg N.M.;  
 RT "The amino acid sequences of the Fd fragments of two human gamma-1  
 heavy chains".  
 RL Biochem. J. 117:641-660(1970).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02089; GIHUCO.  
 DR HSSP; P01825; 7FAB.  
 DR GO; GO:0005576; Extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Glycoprotein; Pyroglutamate carboxylic acid.  
 FT DOMAIN 1 110 IG-LIKE.  
 FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT DISULFID 22 94  
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .).  
 FT NON TER 120 120  
 SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EB98 CRC64;

Query Match 49.3%; Score 300; DB 1; Length 120;  
 Best Local Similarity 52.9%; Pred. No. 2.3e-25;  
 Matches 63; Conservative 16; Mismatches 30; Indels 10; Gaps 3;

QY 2 EESPGVLPKPAQTLSLCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNP 61  
 DB 6 EESPPALVKEPTGITLTCTSGFSLSTGMCVGMIRQPGKLEWLRIMDDDKYNTSL 65  
 62 KSRIANSVDTSENKFSRLNVSVAADTAIVYCARLD-----GYTLIDWGGTLVTSS 114  
 66 ETRLTISKDTSRNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVYSS 120

RESULT 12  
 ID HVA0 MOUSE STANDARD; PRT; 119 AA.  
 AC P01810;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ig heavy chain V region J539.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN (1)  
 RP PRELIMINARY SEQUENCE.  
 RX MEDLINE=79223895; PubMed=111245;  
 RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;  
 RT "Structural evidence for independent joining region gene in  
 immunoglobulin heavy chains from anti-galactan myeloma proteins and  
 its potential role in generating diversity in  
 complementarity-determining regions.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).  
 RL [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RX MEDLINE=88217852; PubMed=3449853;  
 RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,  
 RA Davies D.R.;  
 RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction  
 study at 2.6-A resolution.";  
 RT Proteins 1:74-80(1986).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS GALACTAN.  
 CC PIR; A02080; AVMSJ5.  
 DR PDB; 2FAB; 15-OCT-90.  
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; 3D-structure.  
 FT NON TER 119 119  
 FT STRAND 3 7  
 FT STRAND 10 12  
 FT TURN 14 15  
 FT STRAND 18 25  
 FT STRAND 18 25  
 FT HELIX 29 31  
 FT STRAND 34 39  
 FT TURN 41 42  
 FT STRAND 45 51  
 FT TURN 53 54  
 FT STRAND 58 60  
 FT TURN 62 67  
 FT STRAND 68 72  
 FT STRAND 78 83  
 FT HELIX 88 90  
 FT STRAND 92 100  
 FT TURN 101 103  
 FT STRAND 104 108  
 FT STRAND 112 116  
 SQ SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;

Query Match 48.4%; Score 295; DB 1; Length 119;  
 Best Local Similarity 53.4%; Pred. No. 7.8e-25;  
 Matches 62; Conservative 16; Mismatches 34; Indels 4; Gaps 3;

QY 1 LESGGLVLPKPAQTLSLCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNP 59  
 DB 5 LESGGGLVDPGSGSLKLSCAASFPDSK--YMSWVRQAPGKLEWIGELHPSGINTNTP 62  
 60 SKSRIANSVDTSENKFSRLNVSVAADTAIVYCARLDGYTLID-IMGGTLVTSS 114  
 63 SLKDKFTIRSDNAKSLVLYOMSKVRSDEPTALYYCARLHYGYNAVYGGTTLVTSA 118

RESULT 13  
 ID HVA3 HUMAN STANDARD; PRT; 122 AA.  
 AC P01762;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-III region TRO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE (MYELOMA PROTEIN TRO).  
 RX MEDLINE=76023781; PubMed=809331;  
 RA Kraxin H., Altevogt P., Ruban E., Kortt A., Starosck K.,  
 RA Hilschmann N.;  
 RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),  
 RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III;  
 RT structure of the complete IgA-molecule.";  
 RT Hoppe-Seiler's Z. Physiol. Chem. 356:1337-1342(1975).  
 RL Hopppe-Seiler's Z. Physiol. Chem. 356:1337-1342(1975).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02045; A1HTR.  
 DR HSSP; P01772; 2F84.  
 DR GO; GO:0005576; Extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.



Search completed: February 10, 2004, 18:36:29  
Job time : 6.39091 secs

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Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 84

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114  
 85 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 137

## RESULT 2

ID 09UL73 PRELIMINARY; PRT; 119 AA.

AC 09UL73; PRELIMINARY; PRT; 119 AA.

DT 01-MAY-2000 (TEMBLrel. 13, Created)

DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region (fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

SEQUENCE FROM N.A.

MEDLINE=9827139; PubMed=9614934;

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035041; AAD56277.1; -.

DR HSSP; P01825; 7FAB.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR SMART; SM00407; IG; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1 1

FT SEQUENCE 119 AA; 13219 MW; 1BD8686420EAOBE CRC64;

Query Match 73.3%; Score 446.5; DB 4; Length 119;

Best Local Similarity 74.1%; Pred. No. 2e-39;

Matches 86; Conservative 12; Mismatches 13; Indels 5; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 6 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 63

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 64 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 119

## RESULT 3

ID 096KX8 PRELIMINARY; PRT; 496 AA.

AC 096KX8; PRELIMINARY; PRT; 496 AA.

DT 01-DEC-2001 (TEMBLrel. 19, Created)

DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

SEQUENCE FROM N.A.

TISSUE=Lung;

RA Strauberg R.;

RL EMBL; BC016369; AAH16369.1; -.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR Pfam; PF00047; IG; 4.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Hypothetical protein.

SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 70.9%; Score 432; DB 4; Length 496;

Best Local Similarity 69.2%; Pred. No. 4.2e-37;

Matches 83; Conservative 13; Mismatches 16; Indels 8; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 84

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 85 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 143

Query Match 70.9%; Score 432; DB 4; Length 496;

Best Local Similarity 69.2%; Pred. No. 4.2e-37;

Matches 83; Conservative 13; Mismatches 16; Indels 8; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 61

Db 25 ESGPGLVKEPSETLSLCTVSGSGISSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 82

Qy 62 KSRIMSVDTSSEKPSLRINSVTAAATVAYYCARLDGTLTIDVGGTLYTVSS 114

Db 83 KSRVTSVDSKQPSLRSLSTVTAADTAVYCARLGMGAFDFWGHGTMVSS 139

Query Match 70.6%; Score 430; DB 4; Length 613;

Best Local Similarity 74.4%; Pred. No. 8.9e-37;

Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;





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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035039; AAD56275.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match 59.4%; Score 362; DB 4; Length 122;
Best Local Similarity 61.9%; Pred. No. 1.7e-30;
Matches 73; Conservative 15; Mismatches 24; Indels 6; Gaps 3;

QY 2 ESGPGLVPAQTLISCAVSGSIRSGGYWMIROHKGLEWIGYIHSNTY--YNP 59
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   6 ESGPGLVPSQTLISLCAISGDSVSSNAAWMIKQSPRGLEWIGRTYRSKWNDYRV 65
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 60 SLKSIAMSVPTSEKFSRLNSVTADPTAVYYCAR---LDGYTLIDINGQGLTVTVSS 114
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   66 SVKSLITINPTISKQFSLQNLNSVTPEDTAVYYCARDLELLG-QPDYMGQGLTVTVSS 122
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13.
Q99NG4 PRELIMINARY; PRT; 121 AA.
AC Q99NG4;
DT 01-UN-2001 (TREMBlrel. 17, Created)
DT 01-UN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Placental PHENI.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawlisch H., Frank R., Hennecke M., Baenech M., Soehn B., Arseniev L.,
RA Bausch W., Kola A., Klos A., Koehl J.;
RT "Site-directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Plasmid.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 121 AA; 13255 MW; D293B4B8C8C59D5B CRC64;

Query Match 53.0%; Score 323; DB 11; Length 121;
Best Local Similarity 54.7%; Pred. No. 2.2e-26;
Matches 64; Conservative 19; Mismatches 28; Indels 6; Gaps 2;

QY 2 ESGPGLVPAQTLISCAVSGSIRSGGYWMIROHKGLEWIGYIHSNTYNSL 61

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Db 6 ESGPGLVAPSQSLITCTVSGFPLTSHGV--SWVRQPPGKGLKQLVWIGYIWGDGNTKYSAL 63
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 62 KSRIAMSVPTSEKFSRLNSVTADPTAVYYCAR---LDGYTLIDINGQGLTVTVSS 114
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 64 ISRLISKDMSKSVFLKNSLQTEDTAVYYCAHRYKANYAMDYMGQGLTVTVSS 120
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 14
Q9UL96 PRELIMINARY; PRT; 121 AA.
ID Q9UL96;
AC Q9UL96;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035018; AAD56254.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDJ35 CRC64;

Query Match 52.0%; Score 316.5; DB 4; Length 121;
Best Local Similarity 54.3%; Pred. No. 1.1e-25;
Matches 63; Conservative 14; Mismatches 36; Indels 3; Gaps 1;

QY 2 ESGPGLVPAQTLISCAVSGSIRSGGYWMIROHKGLEWIGYIHSNTYNSL 61
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   6 ESGPGLVPTQTTLTCTFSGFSLTSGMDVGWIRPPGKALFWLALITWDDKRYGPSL 65
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 62 KSRIAMSVPTSEKFSRLNSVTADPTAVYYCARL---DGYTLIDINGQGLTVTVSS 114
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   66 KSRLLTKDYSKQVLDLTMFMDPTAVYYCAHRSKSGDGYFPYMGQGLTVTVSS 121
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 15
Q91X92 PRELIMINARY; PRT; 482 AA.
ID Q91X92;
AC Q91X92;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Unknown (Protein for WGC:18822).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC011181; AAH11181.1; -.
DR InterPro; IPR007110; Ig_1-like.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 : Search time 11.7455 Seconds  
(without alignments)  
410.664 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614  
Sequence: 1 LBSGPGVKKPSQTLSTCTV.....RSDGTVLDNMGGTIVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID                 | Description       |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1          | 507   | 82.6        | 473    | US-09-049-672A-4   | Sequence 4, Appli |
| 2          | 494   | 80.5        | 122    | US-08-360-125-11   | Sequence 11, Appl |
| 3          | 494   | 80.5        | 122    | US-08-450-578-11   | Sequence 11, Appl |
| 4          | 494   | 80.5        | 122    | US-09-017-628-11   | Sequence 11, Appl |
| 5          | 494   | 80.5        | 122    | US-09-014-880-11   | Sequence 11, Appl |
| 6          | 494   | 80.5        | 122    | US-08-450-363-11   | Sequence 11, Appl |
| 7          | 488.5 | 79.6        | 119    | US-09-025-769B-39  | Sequence 39, Appl |
| 8          | 488.5 | 79.6        | 119    | US-09-025-769B-65  | Sequence 65, Appl |
| 9          | 488   | 79.5        | 118    | US-09-025-769B-25  | Sequence 25, Appl |
| 10         | 473.5 | 77.1        | 119    | US-08-360-125-5    | Sequence 5, Appli |
| 11         | 473.5 | 77.1        | 119    | US-08-450-578-5    | Sequence 5, Appli |
| 12         | 473.5 | 77.1        | 119    | US-09-017-628-5    | Sequence 5, Appli |
| 13         | 473.5 | 77.1        | 119    | US-09-014-880-5    | Sequence 5, Appli |
| 14         | 473.5 | 77.1        | 119    | US-08-450-363-5    | Sequence 5, Appli |
| 15         | 459.5 | 74.8        | 142    | US-08-480-774A-2   | Sequence 2, Appli |
| 16         | 458.5 | 74.7        | 250    | US-10-039-785-50   | Sequence 50, Appl |
| 17         | 458   | 74.6        | 244    | US-08-918-148-79   | Sequence 79, Appl |
| 18         | 453   | 73.8        | 118    | US-08-545-809A-116 | Sequence 116, App |
| 19         | 453   | 73.8        | 126    | US-08-276-852-142  | Sequence 142, App |
| 20         | 453   | 73.8        | 126    | US-08-899-575-142  | Sequence 142, App |
| 21         | 453   | 73.8        | 126    | US-08-899-575-142  | Sequence 142, App |
| 22         | 453   | 73.8        | 126    | PCT-US95-08743-142 | Sequence 142, App |
| 23         | 446.5 | 72.7        | 119    | US-08-652-816A-10  | Sequence 10, Appl |
| 24         | 446   | 72.6        | 118    | US-08-545-809A-123 | Sequence 123, App |
| 25         | 446   | 72.6        | 278    | US-09-260-527-3    | Sequence 3, Appli |
| 26         | 445.5 | 72.6        | 123    | US-08-793-450-4    | Sequence 4, Appli |
| 27         | 445.5 | 72.6        | 472    | US-08-793-450-8    | Sequence 8, Appli |

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|----|-------|------|-----|--------------------|-------------------|
| 28 | 445   | 72.5 | 118 | US-09-343-698-6    | Sequence 6, Appli |
| 29 | 443   | 72.1 | 118 | US-08-545-809A-142 | Sequence 142, App |
| 30 | 441   | 71.8 | 244 | US-10-039-785-44   | Sequence 44, Appl |
| 31 | 440.5 | 71.7 | 124 | US-08-478-039-78   | Sequence 78, Appl |
| 32 | 440.5 | 71.7 | 124 | US-08-476-349A-78  | Sequence 78, Appl |
| 33 | 439.5 | 71.6 | 476 | US-08-487-550-12   | Sequence 12, Appl |
| 34 | 439.5 | 71.6 | 476 | US-09-526-098-12   | Sequence 12, Appl |
| 35 | 439   | 71.5 | 118 | US-08-652-816A-13  | Sequence 13, Appl |
| 36 | 438   | 71.3 | 832 | US-08-630-820-7    | Sequence 7, Appli |
| 37 | 436.5 | 71.1 | 219 | US-09-460-384-37   | Sequence 37, Appl |
| 38 | 434.5 | 70.8 | 123 | US-08-137-117D-64  | Sequence 64, Appl |
| 39 | 434.5 | 70.8 | 123 | US-08-436-717-64   | Sequence 64, Appl |
| 40 | 434.5 | 70.8 | 138 | US-08-137-117D-69  | Sequence 69, Appl |
| 41 | 434.5 | 70.8 | 138 | US-08-436-717-69   | Sequence 69, Appl |
| 42 | 432.5 | 70.4 | 98  | US-08-478-039-75   | Sequence 75, Appl |
| 43 | 432.5 | 70.4 | 98  | US-08-476-349A-75  | Sequence 75, Appl |
| 44 | 431.5 | 70.3 | 121 | US-08-275-053-13   | Sequence 13, Appl |
| 45 | 431   | 70.2 | 120 | US-08-057-430A-26  | Sequence 26, Appl |

#### ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
Sequence 4, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Yang, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HERewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ceirone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PR-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANCYTUT01

CLONE: 1513264  
US-09-049-672A-4  
Query Match 82.6%; Score 507; DB 3; Length 473;  
Best Local Similarity 79.8%; Pred. No. 6e-43;  
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;  
QY 2 ESGPGLVKRPSQTLTCTVSGGSIKSGGYWMSVRQPGKGLMIGNIYHSGNTYYPGL 61  
DB 25 ESGPGLVKRPSQTLTCTVSGGSIKSGGYWMSVRQPGKGLMIGNIYHSGNTYYPGL 84  
QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAVYCARSD-----GYTLDMNGGTLVTYSS 114  
DB 85 KSRITMSVDTSKNHFSLRLTSVTADTAVYCARSDVGLRGNGYGMVWGGLTVYSS 143  
RESULT 2  
US-08-360-125-11  
Sequence 11, Application US/08360125  
Patent No. 5767246  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: YOKO HIRAKAWA  
APPLICANT: No. 5767246shiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-11

Query Match 80.5%; Score 494; DB 1; Length 122;  
Best Local Similarity 78.6%; Pred. No. 2.4e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;  
QY 2 ESGPGLVKRPSQTLTCTVSGGSIKSGGYWMSVRQPGKGLMIGNIYHSGNTYYPGL 61  
DB 6 ESGPGLVKRPSQTLTCTVSGGSIKSGGYWMSVRQPGKGLMIGNIYHSGNTYYPGL 65  
QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAVYCARSD-----GYTLDMNGGTLVTYSS 114  
DB 66 KSRITMSVDTSKNHFSLRLTSVTADTAVYCARSDVGLRGNGYGMVWGGLTVYSS 122  
RESULT 3  
US-08-450-578-11  
Sequence 11, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: YOKO HIRAKAWA  
APPLICANT: No. 5837845shiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578

;; FILING DATE: May 25, 1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/360,125  
;; FILING DATE: December 20, 1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/905,534  
;; FILING DATE: June 29, 1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek, Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX:  
;;  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 122 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHEetical:  
;; ANTI-SENSE:  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; ORGANISM:  
;; STRAIN:  
;; INDIVIDUAL ISOLATE:  
;; DEVELOPMENTAL STAGE:  
;; HAPLOTYPE:  
;; TISSUE TYPE:  
;; CELL TYPE: Hybridoma producing human antibody 1-3-1  
;;  
;; ORGANELLE:  
;; IMMEDIATE SOURCE:  
;; LIBRARY:  
;; CLONE:  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT:  
;; MAP POSITION:  
;; UNITS:  
;; FEATURES:  
;; NAME/KEY:  
;; LOCATION:  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION:  
;; PUBLICATION INFORMATION:  
;; AUTHORS:  
;; TITLE:  
;; JOURNAL:  
;; VOLUME:  
;; ISSUE:  
;; PAGES:  
;; DATE:  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:  
;; RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-11

Query Match 80.5%; Score 494; DB 2; Length 122;  
Best Local Similarity 78.6%; Pred. No. 2.4e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Qy 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYWVWROPEPKGLEWIGNTYHSGNTYVNSL 61  
Db 6 ESGPGLVPSQTLSTCTVSGSGSIRSGGYWVWROPEPKGLEWIGNTYHSGNTYVNSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSTVTAADTAIVYVCARSD---GYTLDNWGQGLTVTVSS 114  
Db 66 KSRVITISVDTSKNHFSLRLTSTVTAADTAIVYVCARSD---GYTLDNWGQGLTVTVSS 122

RESULT 4  
US-09-017-628-11  
Sequence 11, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287hiko  
APPLICANT: NAGAIKE, Kazuhiko  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1  
US-09-017-628-11

Query Match 80.5%; Score 494; DB 2; Length 122;  
Best Local Similarity 78.6%; Pred. No. 2.4e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Qy 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYWVWROPEPKGLEWIGNTYHSGNTYVNSL 61  
Db 6 ESGPGLVPSQTLSTCTVSGSGSIRSGGYWVWROPEPKGLEWIGNTYHSGNTYVNSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSTVTAADTAIVYVCARSD---GYTLDNWGQGLTVTVSS 114  
Db 66 KSRVITISVDTSKNHFSLRLTSTVTAADTAIVYVCARSD---GYTLDNWGQGLTVTVSS 122

RESULT 5  
US-09-014-880-11  
Sequence 11, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
US-09-014-860-11

Query Match 80.5%; Score 494; DB 2; Length 122;  
Best Local Similarity 78.6%; Pred. No. 2.4e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQTLSTCTVSGSIRSGGYWVRQPGKGLWIGNIYHSGNTYNNPSL 61  
6 ESGPGLVKSQTLSTCTVSGSIRSGGYWVRQPGKGLWIGNIYHSGNTYNNPSL 65

DB 62 KSRITWSVDTSKNHFSLRLTSVTAADTAVYYCARSD---GYTLDMWGQGLVTVSS 114  
66 KSRVITSVDTSKNQFSLKLSVTAADTAVYYCARSGSYGGYYGMDVWGQGLVTVSS 122

RESULT 6  
US-08-450-363-11  
Sequence 11, Application US/08450363  
Patent No. 6436434  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 6436434hiko ITO  
APPLICANT: Kazuhito NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,363  
FILING DATE: May 25, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLER:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-11

Query Match 80.5%; Score 494; DB 4; Length 122;  
Best Local Similarity 78.6%; Pred. No. 2.4e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQTLSTCTVSGSIRSGGYWVRQPGKGLWIGNIYHSGNTYNNPSL 61  
6 ESGPGLVKSQTLSTCTVSGSIRSGGYWVRQPGKGLWIGNIYHSGNTYNNPSL 65

DB 62 KSRITWSVDTSKNHFSLRLTSVTAADTAVYYCARSD---GYTLDMWGQGLVTVSS 114  
66 KSRVITSVDTSKNQFSLKLSVTAADTAVYYCARSGSYGGYYGMDVWGQGLVTVSS 122

RESULT 7  
US-09-025-769B-39  
Sequence 39, Application US/09025769B  
Patent No. 630064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic

[illegible]

Query Match Similarity 79.6%; Score 488.5; DB 4; Length 119;  
Best Local Similarity 81.9%; Pred. No. 8.4e-42;  
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

RESULT 9  
US-09-025-769B-25  
Sequence 25, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent'n Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-25

Query Match      79.5%; Score 488; DB 4; Length 118;
Best Local Similarity 81.7%; Pred. No. 9.3e-42;
Matches 94; Conservative 7; Mismatches 10; Indels 4; Gaps 2;

QY 2 ESGPGLVKSQTLSTCTVSGSIRSGGYMSWROPFGKLEWIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKSQTLSTCTVSGSIRSGGYMSWROPFGKLEWIGNIYHSGNTYNNPSL 63
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCA-RSDGTTLDNMGCGTLVTYSS 114
DB 64 KSRVITSLDTSKNHFSLRLTSVTAADTAVYYCARGRGGGVFPYWGQGLVTYSS 118

RESULT 10
US-08-360-125-5
Sequence 5, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Tochiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single

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TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5

Query Match      77.1%; Score 473.5; DB 1; Length 119;
Best Local Similarity 78.1%; Pred. No. 2.7e-40;
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 2 ESGPGLVKSQTLSTCTVSGSIRSGGYMSWROPFGKLEWIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKSQTLSTCTVSGSIRSGGYMSWROPFGKLEWIGNIYHSGNTYNNPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-LDNMGCGTLVTYSS 114
DB 66 KSRVITSLDTSKNHFSLRLTSVTAADTAVYYCARSTRLRGADYWGQGLVTYSS 119

RESULT 11
US-08-450-578-5
Sequence 5, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Tochiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
City: Washington

```

```

Qy      2  ESGGVLKPSQTSLTCTVSGGSIRSGGIYSWVRPCKLEIWNIGNYHSGNTYNSPL 61
Db      6  ESGGVLKPSQTSLTCTVSGGSISCGFYNNMIRHPKGKLEIWIYIGSYGSTYNPSL 65
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Qy      62 KSRITMSVDTRSKNHFSLRITSVTAPADNAVYYCASSDGT -LDNMGGGLTVNVSS 114
Db      66 KSRVTISLDRSKSOFSLKLSSLTAADTAIVYYCARSTRLRGADYGQGTMVTVSS 119
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

RESULT 12
US-09-017-628-5
; Sequence 5, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAMA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKI, Kazuhito
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5

Query Match          77.1%; Score 473.5; DB 2; Length 119;
Best Local Similarity 78.1%; Pred. No. 2.7e-40;
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Qy      2  EESGGLVKPSQTSLTCTVSGGSIRSGGIYSWVRPCKLEIWNIGNYHSGNTYNSPL 61
Db      6  EESGGLVKPSQTSLTCTVSGGSISCGFYNNMIRHPKGKLEIWIYIGSYGSTYNPSL 65
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Qy      62 KSRITMSVDTRSKNHFSLRITSVTAPADNAVYYCASSDGT -LDNMGGGLTVNVSS 114
Db      66 KSRVTISLDRSKSOFSLKLSSLTAADTAIVYYCARSTRLRGADYGQGTMVTVSS 119
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

RESULT 13
US-09-014-880-5
; Sequence 5, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS

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SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human  
US-09-014-880-5

Query Match 77.1%; Score 473.5; DB 2; Length 119;  
Best Local Similarity 78.1%; Pred. No. 2.7e-40;  
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYVSWVRQPPGKGLVIGNITHSNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYVSWVRQPPGKGLVIGNITHSNTYNNPSL 65  
QY 62 KSRITMSVDSKMFSLRTSVTAADTAVYYCARSDGYT-LDNMGQGLTVTVSS 114  
DB 66 KSRVITSLDTSKQFSLKLSLTADTAVYYCARSTRLRGADYWGQGTMTVTVSS 119

RESULT 14  
US-08-450-363-5  
Sequence 5, Application US/08450363  
Patent No. 6436434  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Tooshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 6436434hiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
SPECIFICALLY BINDING TO Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,363  
FILING DATE: May 25, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-5

Query Match 77.1%; Score 473.5; DB 4; Length 119;  
Best Local Similarity 78.1%; Pred. No. 2.7e-40;  
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYVSWVRQPPGKGLVIGNITHSNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYVSWVRQPPGKGLVIGNITHSNTYNNPSL 65





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## OM protein - protein search, using sw model

Run on: February 10, 2004, 17:46:18 ; Search time 34.3727 Seconds  
(without alignments)  
526.430 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614  
Sequence: 1 LBSGPGLVKRSQTLSTCTV.....RSDGYTLDMGQGLTVVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 614   | 100.0       | 114    | 23 | ABG30446    |
| 2          | 608   | 99.0        | 114    | 23 | ABG30447    |
| 3          | 546   | 88.9        | 114    | 23 | ABG30445    |
| 4          | 507   | 82.6        | 473    | 22 | AA36206     |
| 5          | 502.5 | 81.8        | 123    | 20 | AAW78433    |
| 6          | 502.5 | 81.8        | 123    | 23 | ABB97976    |
| 7          | 501   | 81.6        | 252    | 23 | ABP45318    |
| 8          | 500.5 | 81.5        | 127    | 22 | AAAG80217   |
| 9          | 500   | 81.4        | 126    | 21 | AA30584     |

|    |       |      |     |    |          |
|----|-------|------|-----|----|----------|
| 10 | 500   | 81.4 | 126 | 23 | ABP54970 |
| 11 | 500   | 81.4 | 251 | 23 | ABG80712 |
| 12 | 500   | 81.4 | 254 | 23 | ABG80713 |
| 13 | 500   | 81.4 | 263 | 23 | ABG80714 |
| 14 | 499.5 | 81.4 | 120 | 22 | AA862775 |
| 15 | 498   | 81.1 | 123 | 21 | AA862745 |
| 16 | 496.5 | 80.9 | 122 | 22 | AA862765 |
| 17 | 495   | 80.8 | 246 | 21 | AAV5126  |
| 18 | 495   | 80.6 | 118 | 20 | AAV6385  |
| 19 | 494.5 | 80.5 | 251 | 24 | ABU19829 |
| 20 | 494   | 80.5 | 172 | 21 | AAV93713 |
| 21 | 493   | 80.3 | 252 | 23 | ABP45983 |
| 22 | 492.5 | 80.2 | 251 | 23 | ABP44979 |
| 23 | 492.5 | 80.2 | 253 | 23 | ABP45608 |
| 24 | 490.5 | 79.9 | 117 | 21 | AAV44615 |
| 25 | 488.5 | 79.6 | 119 | 18 | AAW27554 |
| 26 | 488.5 | 79.6 | 119 | 24 | ABU18676 |
| 27 | 488   | 79.5 | 118 | 20 | AAV6383  |
| 28 | 488   | 79.5 | 139 | 21 | AAV56713 |
| 29 | 487   | 79.3 | 130 | 23 | AAU81273 |
| 30 | 487   | 79.3 | 254 | 23 | ABP45567 |
| 31 | 487   | 79.3 | 256 | 23 | ABP45596 |
| 32 | 484   | 78.8 | 117 | 22 | AAU02540 |
| 33 | 484   | 78.8 | 122 | 14 | AA30145  |
| 34 | 483.5 | 78.7 | 129 | 23 | AAU81275 |
| 35 | 483   | 78.7 | 229 | 21 | AA30593  |
| 36 | 482   | 78.5 | 120 | 22 | AA866415 |
| 37 | 482   | 78.5 | 121 | 23 | AB80711  |
| 38 | 482   | 78.5 | 146 | 24 | ABP57361 |
| 39 | 482   | 78.5 | 154 | 24 | ABP57365 |
| 40 | 480   | 78.2 | 250 | 23 | ABP45537 |
| 41 | 479.5 | 78.1 | 129 | 23 | AAU81276 |
| 42 | 478   | 77.9 | 256 | 23 | ABP45734 |
| 43 | 478   | 77.9 | 487 | 22 | AA890607 |
| 44 | 478   | 77.9 | 487 | 23 | ABG65445 |
| 45 | 477   | 77.7 | 118 | 20 | AAV6386  |

## ALIGNMENTS

|          |  |                                     |
|----------|--|-------------------------------------|
| RESULT 1 | ABG30446   | ABG30446 standard; Protein, 114 AA. |
| ID       | ABG30446   |                                     |
| XX       | ABG30446;  |                                     |
| AC       | 21-OCT-2002 (first entry)                                  |                                     |
| XX       |  |                                     |
| DT       |  |                                     |
| XX       |  |                                     |
| DE       | Human IGE Fab clone 60 heavy chain protein.                |                                     |
| XX       |  |                                     |
| KW       | Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2; |                                     |
| XX       | timothy grass pollen allergen; passive immunotherapy.      |                                     |
| OS       | Homo sapiens.  |                                     |
| XX       |  |                                     |
| FH       | Key  | Location/Qualifiers                 |
| FT       | Region   | 1..26                               |
| FT       |  | /note= "FR1 region"                 |
| FT       | Region   | 27..33                              |
| FT       |  | /note= "CDR1 region"                |
| FT       | Region   | 34..47                              |
| FT       |  | /note= "FR2 region"                 |
| FT       | Region   | 48..63                              |
| FT       |  | /note= "CDR2 protein"               |
| FT       | Region   | 64..95                              |
| FT       |  | /note= "FR3 region"                 |
| FT       | Region   | 96..103                             |
| FT       |  | /note= "CDR2 region"                |
| FT       | Region   | 104..114                            |
| FT       |  | /note= "FR4 region"                 |
| XX       |  |                                     |
| PN       | WO200253595-A1.  |                                     |

Anti-idiotypic VH  
Amyloid peptide co  
Amyloid peptide co  
Human IgG/factor X  
Human HIV-1 monoclonal  
Human HIV-1 monoclonal  
Human HIV-1 monoclonal  
Anti-murine CTLA-4  
Humanised LM609 an  
Human VEGF-2 relat  
The heavy chain of  
Human Blys binding  
Human Blys binding  
Human Blys binding  
Human antibody clo  
Human Ab heavy cha  
Antibody library r  
Humanised LM609 an  
Amino acid sequenc  
Human tKc antibod  
Human Blys binding  
Human Blys binding  
Anti-adipocyte mon  
Mab 1-3-1 variable  
Human tKc antibod  
Variable and first  
Human Fab clone LD  
ebVHIGM MS119D10 h  
Anti-TRAIL-R antib  
Anti-TRAIL-R antib  
Human Blys binding  
Human Blys binding  
Human Blys binding  
Human secreted pro  
Human albumin fusi  
Humanised LM609 an

XX 11-JUL-2002.  
 PD  
 XX  
 PF 27-DEC-2001; 2001WO-SE02908.  
 XX  
 PR 29-DEC-2000; 2000SE-0004892.  
 XX  
 PA (PHMA ) PHARMACIA DIAGNOSTICS AB.  
 XX  
 PI Flicker S, Steinberger P, Kraft D, Valenta R;  
 XX  
 DR WPI; 2002-583604/62.  
 DR N-PSDB; ABK89638.  
 XX  
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for  
 PT environmental allergen detection -  
 XX  
 XX  
 PS Disclosure; Page 37; 45pp; English.  
 CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have anti-allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's  
 CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).  
 CC The group 2 allergen-specific Fabs of the invention may be useful for  
 CC environmental allergen detection and for standardisation of allergen  
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for  
 CC passive immunotherapy of type I allergy, it is also useful for  
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention  
 CC are useful for inter alia, diagnosis, therapy and prevention of type  
 CC I allergy. They are also useful for identification of group 2  
 CC allergen-containing pollen and may be used for blocking the binding of  
 CC grass pollen allergic patients IgE antibodies to Phi p 2. The present  
 CC sequence represents the human IgG fab, clone 60 heavy chain protein of  
 CC the invention.  
 CC  
 SO Sequence 114 AA;  
 Query Match 100.0%; Score 614; DB 23; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-45;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYYSWVRPCKGLKLEWIGNIYHSGNTYYNS 60  
 DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYYSWVRPCKGLKLEWIGNIYHSGNTYYNS 60  
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTADTAAYYCARSDGTYLDNMGGCTLVTVSS 114  
 DB 61 LKSRITMSVDTSKNHFSLRLTSVTADTAAYYCARSDGTYLDNMGGCTLVTVSS 114  
 RESULT 2  
 ABG30447 standard; Protein; 114 AA.  
 ID ABG30447;  
 AC ABG30447;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human IgE Fab clone 100 heavy chain protein.  
 XX  
 KW Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;  
 KM timothy grass pollen allergen; passive immunotherapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..26  
 FT /note= "FRI region"  
 FT 27..33  
 FT /note= "CDR1 region"

FT Region 34..47  
 FT /note= "FR2 region"  
 FT Region 48..63  
 FT /note= "CDR2 protein"  
 FT Region 64..95  
 FT /note= "FR3 region"  
 FT Region 96..103  
 FT /note= "CDR2 region"  
 FT Region 104..114  
 FT /note= "FR4 region"  
 XX  
 XX  
 XX WO200253595-A1.  
 XX  
 PD 11-JUL-2002.  
 XX  
 XX  
 PF 27-DEC-2001; 2001WO-SE02908.  
 XX  
 PR 29-DEC-2000; 2000SE-0004892.  
 XX  
 PA (PHMA ) PHARMACIA DIAGNOSTICS AB.  
 XX  
 PI Flicker S, Steinberger P, Kraft D, Valenta R;  
 XX  
 DR WPI; 2002-583604/62.  
 DR N-PSDB; ABK89639.  
 XX  
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for  
 PT environmental allergen detection -  
 XX  
 XX  
 PS Disclosure; Page 38; 45pp; English.  
 CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have anti-allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's  
 CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).  
 CC The group 2 allergen-specific Fabs of the invention may be useful for  
 CC environmental allergen detection and for standardisation of allergen  
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for  
 CC passive immunotherapy of type I allergy, it is also useful for  
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention  
 CC are useful for inter alia, diagnosis, therapy and prevention of type  
 CC I allergy. They are also useful for identification of group 2  
 CC allergen-containing pollen and may be used for blocking the binding of  
 CC grass pollen allergic patients IgE antibodies to Phi p 2. The present  
 CC sequence represents the human IgG fab, clone 100 heavy chain protein of  
 CC the invention.  
 CC  
 SO Sequence 114 AA;  
 Query Match 99.0%; Score 608; DB 23; Length 114;  
 Best Local Similarity 97.4%; Pred. No. 1.3e-44;  
 Matches 111; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYYSWVRPCKGLKLEWIGNIYHSGNTYYNS 60  
 DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYYSWVRPCKGLKLEWIGNIYHSGNTYYNS 60  
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTADTAAYYCARSDGTYLDNMGGCTLVTVSS 114  
 DB 61 LKSRITMSVDTSKNHFSLRLTSVTADTAAYYCARSDGTYLDNMGGCTLVTVSS 114  
 RESULT 3  
 ABG30445 standard; Protein; 114 AA.  
 ID ABG30445;  
 AC ABG30445;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX

DE Human IGE Fab clone 94 heavy chain protein.  
 XX Human, fab; anti allergic; vaccine; grass pollen; Phi p 2;  
 KM Timothy grass pollen allergen; passive immunotherapy.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Region 1..26 /note= "FRI region"  
 FT Region 27..33 /note= "CDRI region"  
 FT Region 34..47 /note= "FR2 region"  
 FT Region 48..63 /note= "CDR2 protein"  
 FT Region 64..95 /note= "FR3 region"  
 FT Region 96..103 /note= "CDR2 region"  
 FT Region 104..114 /note= "FR4 region"  
 FT Region  
 XX WO200253595-A1.  
 XX 11-JUL-2002.  
 XX 27-DEC-2001; 2001WO-SE02908.  
 XX 29-DEC-2000; 2000SE-0004892.  
 XX (PHAA) PHARMACIA DIAGNOSTICS AB.  
 XX Plucker S, Steinerberger P, Kraft D, Valenta R;  
 P1 WPI; 2002-583604/62.  
 XX N-PSDB; ABK89637.  
 DR  
 XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 FT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for  
 PT environmental allergen detection -  
 XX  
 XX Disclosure; Page 36; 45pp; English.  
 PS  
 XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have anti allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's  
 CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).  
 CC The group 2 allergen-specific Fabs of the invention may be useful for  
 CC environmental allergen detection and for standardisation of allergen  
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for  
 CC passive immunotherapy of type I allergy, it is also useful for  
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention  
 CC are useful for inter alia, diagnosis, therapy and prevention of type  
 CC I allergy. They are also useful for identification of group 2  
 CC allergen-containing pollen and may be used for blocking the binding of  
 CC grass pollen allergic patients IgE antibodies to Phi p 2. The present  
 CC sequence represents the human IgG fab, clone 94 heavy chain protein of  
 CC the invention.  
 CC  
 XX  
 SQ Sequence 114 AA;  
 Query Match 88.9%; Score 546; DB 23; Length 114;  
 Best Local Similarity 89.5%; Pred. No. 2.6e-39;  
 Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

DB  
 61 LKSRITMSVDTSEKPFSLRLNLSVTADTAIVYGCARDLGYTLNMGCGTLVTWSS 114  
 |||||  
 RESULT 4  
 ID AAB36206 standard; protein; 473 AA.  
 XX  
 AC AAB36206;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Human immune system associated protein HISAP-4.  
 XX  
 KM Human, immune system associated protein; HISAP-4; immune disorder;  
 KM infection; autoimmune disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6135941-A.  
 XX  
 PD 24-OCT-2000.  
 XX  
 PF 27-MAR-1998; 98US-0049672.  
 XX  
 PR 27-MAR-1998; 98US-0049672.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;  
 PI Hillman JL, Au-Young J;  
 XX  
 DR WPI; 2001-030926/04.  
 XX  
 DR N-PSDB; AAC66522.  
 XX  
 PT New human immune system associated proteins (HISAP) and polynucleotides  
 PT encoding the HISAP, useful for diagnosing, treating or preventing  
 PT immune or cell proliferative disorders or infections -  
 XX  
 PS Claim 1; Column 53-56; 54pp; English.  
 XX  
 CC The present invention provides the coding and protein sequences for a  
 CC number of human immune system associated proteins (HISAPs). These can be  
 CC used in the diagnosis and treatment of various autoimmune disorders,  
 CC infections and cell proliferation diseases. The diseases include AIDS,  
 CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
 CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
 CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
 CC erythematosus, arteriosclerosis, cirrhosis and cancer.  
 CC  
 XX  
 SQ Sequence 473 AA;  
 Query Match 82.6%; Score 507; DB 22; Length 473;  
 Best Local Similarity 79.8%; Pred. No. 2.4e-35;  
 Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;  
 Oy 2 ESGGGLVPSQTLSTCTVSGSIRSGGYWSWRPPGKLEWIGNYHSGNTYNPDL 61  
 |||||  
 Db 25 ESGGGLVPSQTLSTCTVSGSIRSGGYWSWRPPGKLEWIGNYHSGNTYNPDL 84  
 |||||  
 Oy 62 KSRITMSVDTSEKPFSLRLNLSVTADTAIVYGCARDSD-----GYTLNMGCGTLVTWSS 114  
 |||||  
 Db 85 KSRITMSVDTSEKPFSLRLNLSVTADTAIVYGCARDSDGYTLNMGCGTLVTWSS 143  
 |||||  
 RESULT 5  
 ID AAM78433 standard; Protein; 123 AA.  
 XX  
 AC AAM78433;  
 XX  
 DT 11-MAY-1999 (first entry)  
 XX

[illegible]

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX Homo sapiens.  
 XX OS  
 XX PN WO200202641-A1.  
 XX  
 XX 10-JAN-2002.  
 XX  
 XX PF 15-JUN-2001; 2001WO-US19110.  
 XX  
 XX PR 16-JUN-2000; 2000US-212210P.  
 XX PR 17-OCT-2000; 2000US-240816P.  
 XX PR 16-MAR-2001; 2001US-276248P.  
 XX PR 21-MAR-2001; 2001US-277379P.  
 XX PR 25-MAY-2001; 2001US-293499P.  
 XX  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 XX DR WPI; 2002-114799/15.  
 XX  
 XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for  
 XX the diagnosis and treatment of cancers and immune disorders -  
 XX  
 XX PS Claim 1; Page 1989-1990; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the  
 CC tumor necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
 CC and so may be used to detect and quantitate the presence of BlyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BlyS. They may also be  
 CC administered to treat diseases associated with aberrant BlyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43950-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 252 AA;  
 Query Match 81.6%; Score 501; DB 23; Length 252;  
 Best Local Similarity 78.5%; Pred. No. 4.1e-35;  
 Matches 95; Conservative 10; Mismatches 8; Indels 8; Gaps 2;  
 QY 2 ESGPGLVPRSQTLSTLTGSGSIRSGYRWVROPFGKGLMIGNIYHSNTYNNPSL 61  
 Db 6 ESGPGLVPRSETLSTLTGSGSIRSGYRWVROPFGKGLMIGNIYHSNTYNNPSL 65  
 QY 62 KSRITMSVDTSKNHPSLRITSVTAADTAAYYCARSD-----GYTL---DNMCOGLTWT 113  
 Db 66 KSRVITISVDTSKNQPSLKLSTVTAADTAAYYCARSDYDILITGYPLHAPFIWKGTLVTVS 125  
 QY 114 S 114  
 Db 126 S 126

DT 22-JAN-2002 (first entry)  
 XX  
 XX DE Human autoantibody MICA-6 variable region light chain.  
 XX  
 KW Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;  
 KW glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;  
 KW polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;  
 KW variable region; light chain; MICA-6.  
 XX  
 XX OS Homo sapiens.  
 XX PN Ep1149914-A2.  
 XX  
 XX PD 31-OCT-2001.  
 XX  
 XX PF 29-MAR-2001; 2001EP-0107702.  
 XX  
 XX PR 10-APR-2000; 2000DE-1017782.  
 XX PR 25-MAY-2000; 2000DE-1025840.  
 XX  
 XX PA (LABO-) LABOR KOCH MERK GMBH.  
 XX  
 XX PI Richter W, Rickert M, Rapp I, Dangel W;  
 XX  
 XX DR WPI; 2001-640702/74.  
 XX DR N-PSDB; AA168766.  
 XX  
 XX PT New fusion protein, useful for diagnosis of diabetes type I and other  
 XX metabolic diseases, is reactive with autoantibodies against both  
 XX glutamate decarboxylase and islet cell antigen -  
 XX  
 XX PS Disclosure; Page 35-36; 68pp; German.  
 XX  
 CC This invention describes a novel fusion protein (I) that has, at its  
 CC N-terminus, one or more epitopes that bind specifically to autoantibodies  
 CC (Aab) against the islet cell antigen IA2 and, at its C-terminus, one or  
 CC more epitopes that bind specifically to autoantibodies (Ab) directed against  
 CC the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding  
 CC it, vectors containing (II) and transformed cells, are useful for  
 CC diagnosis and prognosis of diabetes mellitus type I, stiff-man syndrome,  
 CC polyglandular autoimmune syndrome or other autoimmune conditions  
 CC associated with Aab against GAD65 or IA2. (I) provides a rapid and simple  
 CC diagnosis of high specificity and sensitivity, capable of recognizing  
 CC antibodies against both IA2 and GAD65, simultaneously. Unlike known  
 CC fusions, where the GAD65 component is at the N-terminus, (I) contains  
 CC correctly folded conformational epitopes that can react with most MICA  
 CC autoantibodies. This sequence represents the human autoantibody MICA-6  
 CC variable region light chain used in the method of the invention.  
 XX  
 SQ Sequence 127 AA;  
 Query Match 81.5%; Score 500.5; DB 22; Length 127;  
 Best Local Similarity 78.0%; Pred. No. 2.2e-35;  
 Matches 96; Conservative 7; Mismatches 11; Indels 9; Gaps 1;  
 QY 1 LESGPGLVKPSQTLSTLTGSGSIRSGYRWVROPFGKGLMIGNIYHSNTYNNPS 60  
 Db 5 LESGPGLVKPSSETLSTLTGSGSIRSGYRWVROPFGKGLMIGNIYHSNTYNNPS 64  
 QY 61 LKSRITMSVDTSKNHPSLRITSVTAADTAAYYCARSD-----DGYTLNMGOGTLT 111  
 Db 65 LKSRVITISVDTSKNQPSLKLSTVTAADTAAYYCARSDYDILITGYPLHAPFIWKGTLVTV 124  
 QY 112 VSS 114  
 Db 125 VSS 127

RESULT 8  
 AAG80217  
 ID AAG80217 standard; Protein; 127 AA.  
 XX  
 AC AAG80217;  
 XX

RESULT 9  
 AAB30584  
 ID AAB30584 standard; Protein; 126 AA.  
 XX  
 AC AAB30584;  
 XX

```

XX
DT 19-MAR-2001 (first entry)
XX
XX A human variable heavy chain region of anti-IgE antibody.
DE
XX Anti-idiotypic antibody; C-epsilon3 region; immunoglobulin E; IgE;
XX anti-IgE antibody; mimotope; allergy; asthma; atopic dermatitis;
XX rhinitis; chronic urticaria; food allergy; IgE-mediated disease;
XX passive immunisation.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 30..37
FT Region /note= "complementarity determining region 1"
FT Region 51..67
FT Region /note= "complementarity determining region 2"
FT Region 100..115
FT Region /note= "complementarity determining region 3"
XX
XX WO200063252-A1.
XX
XX 26-OCT-2000.
XX
XX 12-APR-2000; 2000WO-EP03288.
XX
XX 14-APR-1999; 99GB-0008533.
XX
XX (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GRS MBH.
XX
XX Kricsek F, Stadler B, Vogel M;
XX
XX WPI; 2000-687161/67.
XX
XX N-PSDB; AAC62336.
XX
XX Novel anti-idiotypic antibody against antibodies which inhibit binding
XX of immunoglobulin E to its high affinity receptor, useful in vaccines
XX for treating diseases such as allergy, rhinitis, atopic dermatitis -
XX
XX Claim 4; Fig 5c; 73pp; English.
XX
XX The present sequence represents a human variable heavy chain region of
XX an anti-idiotypic antibody that interferes with the binding of the
XX C-epsilon3 region of immunoglobulin (Ig)E to the high affinity receptor
XX for IgE, i.e. and anti-IgE antibody. Such an antibody is referred to
XX as a mimotope. The anti-IgE antibody fragment is used as a vaccine, and
XX as a pharmaceutical for treating IgE-mediated diseases such as allergy,
XX in particular asthma, atopic dermatitis, rhinitis, chronic urticaria and
XX food allergies. It is also used to treat IgE-mediated diseases. It is
XX also used for raising polyclonal or monoclonal antibodies. The polyclonal
XX or monoclonal antibodies obtained are useful for treating IgE-mediated
XX diseases by passive immunisation.
XX
XX Sequence 126 AA;
SQ
Query Match 81.4%; Score 500; DB 21; Length 126;
Best Local Similarity 78.7%; Pred. No. 2.4e-35;
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;
QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYYMSWRQPPGKGLWIGNIYHSGNTYYNPS 60
DB 5 LESGPGLVKPSQTLSTCTVSGSIRSGYYMTWRQPPGKGLWIGNIYHSGNTYYNPS 64
QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDG-----YTLDNMGQGTLLTV 112
DB 65 LKSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDG-----YTLDNMGQGTLLTV 124
QY 113 SS 114
DB 125 SS 126

```

```

RESULT 10
ID ABP54970
XX ABP54970 standard; Protein; 126 AA.
XX
XX AC ABP54970;
XX
XX 14-JAN-2003 (first entry)
XX
XX Anti-idiotypic VH sequence mimicking IgE conformational epitope.
DE
XX Human; IgE; immunoglobulin; antibody; epitope; mimotope;
XX lactic acid bacterium; allergy; vaccine; antiallergic;
XX dermatological; antiinflammatory; anti-idiotypic.
XX
XX Homo sapiens.
OS
XX
XX EP1239032-A1.
XX
XX 11-SEP-2002.
XX
XX 02-MAR-2001; 2001EP-0105138.
XX
XX 02-MAR-2001; 2001EP-0105138.
XX
XX (NEST ) SOC PROD NESTLE SA.
XX
XX Stadler BM, Vogel M, Germond J, Fritsche R;
XX
XX WPI; 2002-684058/74.
XX
XX New bacterial strain of lactic acid bacterium group, expressing surface
XX polypeptide which contains peptide sequence mimicking at least part of
XX conformational epitope of immunoglobulin E, useful for treating allergy
XX
XX Claim 4; Page 5; 19pp; English.
XX
XX The present invention relates to recombinant strains of lactic
XX acid bacteria that express surface polypeptides containing
XX peptides (mimotopes) or antibody fragments which mimic at least
XX part of a conformational epitope of an IgE molecule. These are
XX used in food and pharmaceutical compositions, in particular
XX vaccines, for the treatment or prevention of an allergic reaction
XX involving IgE, such as rhinitis, atopic dermatitis and erythema.
XX The mimotope peptides or antibody fragments are obtained by
XX screening random peptide and human Fab antibody phage display
XX libraries with an antibody directed to the Fc part of IgE. The
XX present sequence is the protein sequence of an anti-idiotypic Fab
XX heavy chain variable region (VH) sequence mimicking an IgE
XX conformational epitope.
XX
XX Sequence 126 AA;
SQ
Query Match 81.4%; Score 500; DB 23; Length 126;
Best Local Similarity 78.7%; Pred. No. 2.4e-35;
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;
QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYYMSWRQPPGKGLWIGNIYHSGNTYYNPS 60
DB 5 LESGPGLVKPSQTLSTCTVSGSIRSGYYMTWRQPPGKGLWIGNIYHSGNTYYNPS 64
QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDG-----YTLDNMGQGTLLTV 112
DB 65 LKSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDG-----YTLDNMGQGTLLTV 124
QY 113 SS 114
DB 125 SS 126

```

```

RESULT 11
ID ABG80712
ABG80712 standard; Peptide; 251 AA.

```



XX ABG80712;  
 AC 29-NOV-2002 (first entry)  
 DT  
 XX  
 XX Amyloid peptide containing an attachment site #2.  
 DE  
 XX Molecular antigen array; vaccine; antigen; antimicrobial; mutant;  
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutein;  
 KM graft versus host disease; IGH-mediated allergic reaction; anaphylaxis;  
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;  
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;  
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 KM enterokinase; cysteine-containing linker.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200256907-A2.  
 PN  
 XX  
 PD 25-JUL-2002.  
 XX  
 XX 21-JAN-2002; 2002WO-IB00168.  
 PF  
 XX 19-JAN-2001; 2001US-262379P.  
 PR 04-MAY-2001; 2001US-288549P.  
 PR 05-OCT-2001; 2001US-326998P.  
 PR 07-NOV-2001; 2001US-331045P.  
 XX  
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (NOVS) NOVARTIS PHARMA AG.  
 PA (MAUR/) MAURER P.  
 PA (LECH/) LECHNER F.  
 PA (ORTM/) ORTMANN R.  
 PA (LUBO/) LUBOEND R.  
 PA (STAU/) STAUFENBIEL M.  
 PA (FREY/) FREY P.  
 XX  
 PI Maurer P, Lechner F, Ortmann R, Luegend R, Staufenbiel M, Frey P;  
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;  
 DR WPI; 2002-636514/68.  
 XX  
 PT Molecular antigen array used in the production of vaccines for  
 PT infectious diseases -  
 XX  
 XX Claim 38; Page 227; 418pp; English.  
 XX  
 XX The invention relates to a composition comprising: (a) a non-natural  
 CC molecular scaffold comprising: (i) a core particle selected from:  
 CC (1) a core particle of a non-natural origin; and (2) a core particle of  
 CC natural origin; and (ii) an organism comprising at least one first  
 CC attachment site, where the organism is connected to the core particle by  
 CC at least one covalent bond; (b) an antigen or antigenic determinant with  
 CC at least one second attachment site, where the antigen or antigenic  
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and  
 CC where the second attachment site is selected from: (i) an attachment site  
 CC not naturally occurring with the antigen or antigenic determinant; and  
 CC (ii) an attachment site naturally occurring with the antigen or  
 CC antigenic determinant, where the second attachment site is capable of  
 CC association through at least one non-peptide bond to the first attachment  
 CC site; and where the antigen or antigenic determinant and the scaffold  
 CC interact through the association to form an ordered and repetitive  
 CC antigen array. Also included is a process for producing a non-naturally  
 CC occurring ordered and repetitive antigen array. The composition is used  
 CC in immunisation and as a vaccine for diseases such as influenza,  
 CC graft versus host disease, IGH-mediated allergic reactions, anaphylaxis,  
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic  
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's

CC disease, systemic lupus erythematosus, inflammatory immune diseases,  
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's  
 CC disease, osteoporosis and infectious diseases. The present sequence is  
 CC a modified antigen for use in the array of the invention. The antigen is  
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a  
 CC Cysteine-containing N- or C-terminal linker peptide which serves as the  
 CC attachment point to a virus like particle or bacterial protein (the  
 CC scaffold protein).  
 CC  
 XX Sequence 251 AA;  
 XX  
 SO  
 Query Match 81.4%; Score 500; DB 23; Length 251;  
 Best Local Similarity 78.7%; Pred. No. 5e-35;  
 Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;  
 QY 1 LKSGPLVKSQSLTCTVSGGSIIRSGGYWVWPPGKGLMIGNIYHSGNTYVNS 60  
 DB 20 LKSGPLVKSQSLTCTVSGGSIIRSGGYWVWPPGKGLMIGNIYHSGNTYVNS 79  
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-----YTLDMWGGSTLVTV 112  
 DB 80 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-----YTLDMWGGSTLVTV 139  
 QY 113 SS 114  
 DB 140 SS 141  
 XX  
 XX  
 XX RESULT 12  
 XX ABG80713  
 ID ABG80713 standard; Peptide: 254 AA.  
 XX  
 XX ABG80713;  
 AC 29-NOV-2002 (first entry)  
 DT  
 XX  
 XX Amyloid peptide containing an attachment site #3.  
 DE  
 XX Molecular antigen array; vaccine; antigen; antimicrobial; mutant;  
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutein;  
 KM graft versus host disease; IGH-mediated allergic reaction; anaphylaxis;  
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;  
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;  
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 KM enterokinase; cysteine-containing linker.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO200256907-A2.  
 PN  
 XX 25-JUL-2002.  
 XX  
 XX 21-JAN-2002; 2002WO-IB00168.  
 PF  
 XX 19-JAN-2001; 2001US-262379P.  
 PR 04-MAY-2001; 2001US-288549P.  
 PR 05-OCT-2001; 2001US-326998P.  
 PR 07-NOV-2001; 2001US-331045P.  
 XX  
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (NOVS) NOVARTIS PHARMA AG.  
 PA (MAUR/) MAURER P.  
 PA (LECH/) LECHNER F.  
 PA (ORTM/) ORTMANN R.  
 PA (LUBO/) LUBOEND R.  
 PA (STAU/) STAUFENBIEL M.

PA (FRET/) FREY P.  
 XX Maurer P, Lechner F, Ottmann R, Luegend R, Staufenbiel M, Frey P;  
 PI Renner WA, Bachmann M, Tisot A, Sebbel P, Piossek C;  
 XX WPI; 2002-636514/68.  
 DR  
 XX Molecular antigen array used in the production of vaccines for  
 PT infectious diseases -  
 XX  
 PS Claim 38; Page 227; 418pp; English.  
 XX  
 CC The invention relates to a composition comprising: (a) a non-natural  
 CC molecular scaffold comprising: (i) a core particle selected from:  
 CC (1) a core particle of a non-natural origin; and (2) a core particle of  
 CC natural origin; and (ii) an organiser comprising at least one first  
 CC attachment site, where the organiser is connected to the core particle by  
 CC at least one covalent bond; (b) an antigen or antigenic determinant with  
 CC at least one second attachment site, where the antigen or antigenic  
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and  
 CC where the second attachment site is selected from: (i) an attachment site  
 CC not naturally occurring with the antigen or antigenic determinant; and  
 CC (ii) an attachment site naturally occurring with the antigen or  
 CC antigenic determinant, where the second attachment site is capable of  
 CC association through at least one non-peptide bond to the first attachment  
 CC site; and where the antigen or antigenic determinant and the scaffold  
 CC interact through the association to form an ordered and repetitive  
 CC antigen array. Also included is a process for producing a non-naturally  
 CC occurring ordered and repetitive antigen array. The composition is used  
 CC in immunisation and as a vaccine for diseases such as influenza,  
 CC graft versus host disease, IGE-mediated allergic reactions, anaphylaxis,  
 CC acute respiratory distress syndrome (ARDS), Crohn's disease, allergic  
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's  
 CC disease, systemic lupus erythematosus, inflammatory immune diseases,  
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's  
 CC disease, osteoporosis and infectious diseases. The present sequence is  
 CC a modified antigen for use in the array of the invention. The antigen is  
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a  
 CC cysteine-containing N- or C-terminal linker peptide which serves as the  
 CC attachment point to a virus like particle or bacterial protein (the  
 CC scaffold protein).  
 XX  
 XX Sequence 254 AA;  
 SQ  
 Query Match 81.4%; Score 500; DB 23; Length 254;  
 Best local Similarity 78.7%; Pred. No. 5e-35;  
 Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;  
 QY 1 LBSGPGILVPSQTLSTLTCTVSGSIRSGYVWVROPKGLFWMIGNITHSGNTYVNP 60  
 DB 20 LBSGPGILVPSQTLSTLTCTVSGSIRSGYVWVROPKGLFWMIGNITHSGNTYVNP 79  
 QY 61 LKSRITMSVDTSKNHFSLRLTSVAADTAVYVYCCRSNG-----YTLNMGCGTLVTV 112  
 DB 80 LKSRITMSVDTSKNHFSLRLTSVAADTAVYVYCCRSNG-----YTLNMGCGTLVTV 139  
 QY 113 SS 114  
 DB 140 SS 141  
 RESULT 13  
 ABG80714  
 ID ABG80714 standard; Protein: 263 AA.  
 XX  
 AC ABG80714;  
 XX  
 DT 29-NOV-2002 (first entry)  
 XX  
 DE Human IgG/factor Xa cleavage site fusion protein from pCep--Xa-Fc\*.

KW Molecular antigen array; vaccine; antigen; antimicrobial; mutant;  
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutagen;  
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;  
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;  
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;  
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 KW enterokinase; cysteine-containing linker.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200256907-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 21-JAN-2002; 2002WO-1B00168.  
 XX  
 PR 19-JAN-2001; 2001US-262379P.  
 PR 04-MAY-2001; 2001US-288549P.  
 PR 05-OCT-2001; 2001US-326998P.  
 PR 07-NOV-2001; 2001US-331045P.  
 XX  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (NOVS) NOVARTIS PHARMA AG.  
 PA (MAUR/) MAURER P.  
 PA (LECH/) LECHNER F.  
 PA (ORTM/) ORTMANN R.  
 PA (LUEC/) LUEDEMANN R.  
 PA (STAU/) STAUFENBIEL M.  
 PA (FRET/) FREY P.  
 XX  
 PI Maurer P, Lechner F, Ottmann R, Luegend R, Staufenbiel M, Frey P;  
 PI Renner WA, Bachmann M, Tisot A, Sebbel P, Piossek C;  
 XX  
 DR WPI; 2002-636514/68.  
 DR N-PSDB; ABS6508.  
 XX  
 PT Molecular antigen array used in the production of vaccines for  
 PT infectious diseases -  
 XX  
 PS Example 1; Fig 1; 418pp; English.  
 XX  
 CC The invention relates to a composition comprising: (a) a non-natural  
 CC molecular scaffold comprising: (i) a core particle selected from:  
 CC (1) a core particle of a non-natural origin; and (2) a core particle of  
 CC natural origin; and (ii) an organiser comprising at least one first  
 CC attachment site, where the organiser is connected to the core particle by  
 CC at least one covalent bond; (b) an antigen or antigenic determinant with  
 CC at least one second attachment site, where the antigen or antigenic  
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and  
 CC where the second attachment site is selected from: (i) an attachment site  
 CC not naturally occurring with the antigen or antigenic determinant; and  
 CC (ii) an attachment site naturally occurring with the antigen or  
 CC antigenic determinant, where the second attachment site is capable of  
 CC association through at least one non-peptide bond to the first attachment  
 CC site; and where the antigen or antigenic determinant and the scaffold  
 CC interact through the association to form an ordered and repetitive  
 CC antigen array. Also included is a process for producing a non-naturally  
 CC occurring ordered and repetitive antigen array. The composition is used  
 CC in immunisation and as a vaccine for diseases such as influenza,  
 CC graft versus host disease, IGE-mediated allergic reactions, anaphylaxis,  
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic  
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's  
 CC disease, systemic lupus erythematosus, inflammatory immune diseases,  
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's  
 CC disease, osteoporosis and infectious diseases. The present sequence is  
 CC a modified antigen for use in the array of the invention. The antigen is

modified to possess a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N- or C-terminal linker peptide which serves as the attachment point to a virus like particle or bacterial protein (the scaffold protein).

Sequence 263 AA;

Query Match 81.4%; Score 500; DB 23; Length 263;

Best Local Similarity 78.7%; Pred. No. 5.2e-35;

Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYMSWVRQPGKLEWIGNYHSGNTYVNS 60  
DB 20 LESGPGLVKPSQTLSTCTVSGSIRSGGYMSWVRQPGKLEWIGNYHSGNTYVNS 79  
QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAAYVVCARSDG-----YTLDMNGGTLVTV 112  
DB 80 LKSRITMSVDTSKNHFSLRLTSVTAADTAAYVVCARSDGGLYPPYYIDVWGCTGTVTV 139  
QY 113 SS 114  
DB 140 SS 141

#### RESULT 14

AAB62775 ID AAB62775 standard; Protein, 120 AA.

AC AAB62775;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

KW envelope glycoprotein; gp120; diagnosis.

XX Homo sapiens.

PN WO200100678-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-US17327.

PR 30-JUN-1999; 99US-0141701.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Watkins BA, Reitz MS;

XX WPI; 2001-112438/12.

DR N-PSDB; AAF29076.

PT Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1

PT infected mammal

PS Claim 1; Page 69; 81pp; English.

XX The present invention provides the protein and coding sequences for the

CC variable regions of human monoclonal antibodies which are immunoreactive

CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

CC These can be used in diagnosis and therapy of HIV-1 infection.

XX Sequence 120 AA;

Query Match 81.4%; Score 499.5; DB 22; Length 120;

Best Local Similarity 82.8%; Pred. No. 2.5e-35;

Matches 96; Conservative 8; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGGGLVPSQTLSTCTVSGSIRSGGYMSWVRQPGKLEWIGNYHSGNTYVNSL 61

DB 7 ESGGGLVPSQTLSTCTVSGSIRSGGYMSWVRQPGKLEWIGNYHSGNTYVNSL 66

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVVCARSDG---DGYTLDMNGGTLVTVSS 114

DB 67 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVVCARSDGGLYPPYYIDVWGCTGTVTVSS 120

#### RESULT 15

AAB62745 ID AAB62745 standard; Protein, 123 AA.

AC AAB62745;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody SEQ ID NO: 44.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

KW envelope glycoprotein; gp120; diagnosis.

XX Homo sapiens.

PN WO200100678-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-US17327.

PR 30-JUN-1999; 99US-0141701.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Watkins BA, Reitz MS;

XX WPI; 2001-112438/12.

DR N-PSDB; AAF29046.

PT Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1

PT infected mammal

PS Claim 1; Page 50; 81pp; English.

XX The present invention provides the protein and coding sequences for the

CC variable regions of human monoclonal antibodies which are immunoreactive

CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

CC These can be used in diagnosis and therapy of HIV-1 infection.

XX Sequence 123 AA;

Query Match 81.1%; Score 498; DB 22; Length 123;

Best Local Similarity 80.3%; Pred. No. 3.5e-35;

Matches 94; Conservative 10; Mismatches 9; Indels 4; Gaps 1;

QY 2 ESGGGLVPSQTLSTCTVSGSIRSGGYMSWVRQPGKLEWIGNYHSGNTYVNSL 61

DB 7 ESGGGLVPSQTLSTCTVSGSIRSGGYMSWVRQPGKLEWIGNYHSGNTYVNSL 66

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVVCARSDG---DGYTLDMNGGTLVTVSS 114

DB 67 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVVCARSDGGLYPPYYIDVWGCTGTVTVSS 123

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Job time : 35.3727 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:39:30 ; Search time 26.2545 Seconds

(without alignments)  
909.160 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LESGRLVKSQTLSTLCTV.....RSDGYTLDNWGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
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| 1          | 614   | 100.0       | 114    | 15    | US-10-027-725A-8  |
| 2          | 600   | 97.7        | 114    | 15    | US-10-027-725A-9  |
| 3          | 546   | 88.9        | 114    | 15    | US-10-027-725A-7  |
| 4          | 510.5 | 83.1        | 121    | 12    | US-10-309-762-152 |
| 5          | 510   | 83.1        | 118    | 12    | US-10-309-762-138 |
| 6          | 509.5 | 82.0        | 123    | 12    | US-10-309-762-10  |
| 7          | 507.5 | 82.7        | 125    | 12    | US-10-309-762-11  |
| 8          | 507   | 82.6        | 120    | 12    | US-10-309-762-13  |
| 9          | 507   | 82.6        | 120    | 12    | US-10-309-762-144 |
| 10         | 507   | 82.6        | 122    | 11    | US-10-309-762-147 |
| 11         | 506   | 82.4        | 121    | 11    | US-09-972-656-80  |
| 12         | 505.5 | 82.3        | 121    | 12    | US-10-309-762-151 |
| 13         | 504.5 | 82.2        | 117    | 12    | US-10-330-613-13  |
| 14         | 504.5 | 82.2        | 117    | 12    | US-10-330-530-13  |
| 15         | 503.5 | 82.0        | 119    | 12    | US-10-309-762-140 |

|    |       |      |     |    |                    |                   |
|----|-------|------|-----|----|--------------------|-------------------|
| 16 | 502.5 | 81.8 | 123 | 12 | US-10-309-762-12   | Sequence 12, Appl |
| 17 | 502   | 81.8 | 124 | 12 | US-10-309-762-75   | Sequence 75, Appl |
| 18 | 502   | 81.8 | 143 | 12 | US-10-309-762-96   | Sequence 96, Appl |
| 19 | 501   | 81.6 | 252 | 11 | US-09-880-748-1329 | Sequence 1329, Ap |
| 20 | 500   | 81.4 | 120 | 12 | US-10-309-762-128  | Sequence 128, App |
| 21 | 500   | 81.4 | 120 | 12 | US-10-309-762-139  | Sequence 139, App |
| 22 | 500   | 81.4 | 121 | 12 | US-10-308-817-137  | Sequence 137, App |
| 23 | 500   | 81.4 | 126 | 10 | US-09-974-449-6    | Sequence 6, Appl  |
| 24 | 499   | 81.3 | 116 | 12 | US-10-309-762-127  | Sequence 127, App |
| 25 | 498.5 | 81.2 | 125 | 12 | US-10-309-762-127  | Sequence 8, Appl  |
| 26 | 498.5 | 81.2 | 125 | 12 | US-10-309-762-16   | Sequence 16, Appl |
| 27 | 497.5 | 81.0 | 119 | 12 | US-10-309-762-131  | Sequence 131, App |
| 28 | 497   | 80.9 | 110 | 12 | US-10-309-762-74   | Sequence 74, Appl |
| 29 | 496.5 | 80.9 | 123 | 12 | US-10-309-762-9    | Sequence 9, Appl  |
| 30 | 496.5 | 80.9 | 127 | 12 | US-10-309-762-14   | Sequence 14, Appl |
| 31 | 495.5 | 80.7 | 113 | 12 | US-10-309-762-148  | Sequence 148, App |
| 32 | 495   | 80.6 | 118 | 12 | US-10-078-7578-52  | Sequence 52, Appl |
| 33 | 494.5 | 80.5 | 125 | 12 | US-10-309-762-153  | Sequence 153, App |
| 34 | 494.5 | 80.5 | 251 | 12 | US-10-120-414-75   | Sequence 75, Appl |
| 35 | 494   | 80.5 | 172 | 15 | US-10-153-382-21   | Sequence 21, Appl |
| 36 | 493.5 | 80.4 | 117 | 12 | US-10-330-613-5    | Sequence 5, Appl  |
| 37 | 493.5 | 80.4 | 117 | 12 | US-10-330-530-5    | Sequence 5, Appl  |
| 38 | 493.5 | 80.4 | 123 | 12 | US-10-309-762-17   | Sequence 17, Appl |
| 39 | 493   | 80.3 | 252 | 11 | US-09-880-748-1994 | Sequence 1994, Ap |
| 40 | 492.5 | 80.2 | 119 | 12 | US-10-309-762-143  | Sequence 143, App |
| 41 | 492.5 | 80.2 | 251 | 11 | US-09-880-748-990  | Sequence 990, App |
| 42 | 492.5 | 80.2 | 253 | 11 | US-09-880-748-1619 | Sequence 1619, Ap |
| 43 | 491.5 | 80.0 | 117 | 12 | US-10-309-762-22   | Sequence 22, Appl |
| 44 | 491.5 | 80.0 | 123 | 12 | US-10-309-762-18   | Sequence 18, Appl |
| 45 | 491.5 | 80.0 | 123 | 12 | US-10-309-762-19   | Sequence 19, Appl |

## ALIGNMENTS

RESULT 1  
US-10-027-725A-8  
; Sequence 8, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use thereof  
; FILE REFERENCE: 25401.4  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US/10/027,725A  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-8

Query Match 100.0%; Score 614; DB 15; Length 114;  
Best Local Similarity 100.0%; Pred. No. 2.5e-49;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGRLVKSQTLSTLCTVSGSIRSGLYWSWVROPFGKLEWIGNIYHSGWTVNPS 60  
DB 1 LESGRLVKSQTLSTLCTVSGSIRSGLYWSWVROPFGKLEWIGNIYHSGWTVNPS 60  
QY 61 LKSRITMSVDTSKNHFSLRTSVTAADTAIVYVCARSDGYTLDNWGQGLTVTVSS 114  
DB 61 LKSRITMSVDTSKNHFSLRTSVTAADTAIVYVCARSDGYTLDNWGQGLTVTVSS 114  
RESULT 2  
US-10-027-725A-9  
; Sequence 9, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:

```

APPLICANT: Flicker, Sabine
TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
FILE REFERENCE: 25401-4
CURRENT APPLICATION NUMBER: US/10/027,725A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/259,436
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-027-725A-9

```

|                           |       |                   |          |            |
|---------------------------|-------|-------------------|----------|------------|
| Query Match               | 97.7% | Score 600         | DB 15    | Length 114 |
| Best Local Similarity     | 96.5% | Pred. No. 4.8e+48 |          |            |
| Matches 110, Conservative | 3     | Mismatches 1      | Indels 0 | Gaps 0     |

**Oy**

I LESGPELVKPSQTLSTLTCTVSGSIRSGGYWMSWRQPCKGLEMIIGNIYHSGNTYYNPS 60  
|||||  
||||| : |||||  
|||||  
**Db**

I LESGPGLVKPQQLSLTCTVSGGSIRSGGYWMSWIRQPPCKGLEMIIGIYHSGNTYYNPS 60  
|||||

```

Qy      61 LKSRITMSVDTSKNHFSRLRITSYTAADTAVYYCARSDGYTLDMWGQGILVTVSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 LKSRVTMSVDTSKNHFSRLRSSYTAADTAVYYCARSDGYTLDMWGQGLVTVSS 114

```

```

RESULT 3
US-10-027-725A-7
; Sequence 75, Application US/100272725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific Ige-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

```

| Query Match           | 88.9%;          | Score 546;  | DB 15;    | Length 114; |
|-----------------------|-----------------|---|-----------|-------------|
| Best Local Similarity | 89.5%;          | Pred. No. 4.6e-43;                                      |           |             |
| Matches 102;          | Conservative 4; | Mismatches 8;   | Indels 0; | Gaps 0;     |
| Qy                    | 1               | LESRGVLKPSQTLSTLCTVSGSIRSGGYWSVRQPPGKGLMEIGNIYHSGNTYNS  | 60        |             |
|                       |                 | :     :     :     :     :     :     :     :     :     : |           |             |
| Db                    | 1               | LESRGVLKPAQTLSTLCAVSGSGIRSGGYWSMIRHPGKGLMEIGIYHSGNTYNS  | 60        |             |
| Qy                    | 61              | LKSRITWSVDTSKNHFSRLTSVTAADPAVYYCCARSQGYTLDMNGOGTLTVSS   | 114       |             |
|                       |                 | :     :     :     :     :     :     :     :     :       |           |             |
| Db                    | 61              | LKSRITWSVDTSKNHFSRLTSVTAADPAVYYCCARLDGYTLDMNGOGTLTVSS   | 114       |             |

```

RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Jan
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A

```

```

; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-309-762-152

```

|                       |       |              |         |            |    |        |     |
|-----------------------|-------|--------------|---------|------------|----|--------|-----|
| Query Match           | 83.1% | Score        | 510.5   | DB         | 12 | Length | 121 |
| Best Local Similarity | 82.6% | Pred. No.    | 9.2e-40 |            |    |        |     |
| Matches               | 96    | Conservative | 8       | Mismatches | 9  | Indels | 3   |
|                       |       |              |         |            |    | Gaps   | 1   |

```

0y      2 ESGPELVKPSQTLSTCTVSGGSIIRGGGYWVWROPPGKGLEIMIGNIYHSGNTYYNPSL 61
        |||||
db      6 ESGPELVKPSQTLSTCTVSGGSIIRGGGYWVWIRQHPGKGLEIMIGIYIYSGSTYYNPST 65

```

```

QY      62 KSRITMSVDTSKDNHFSLRLTSTVTAADTAVYYCAASD--GYTLDNNGQGLTVTVSS 114
      |||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
DB      66 KSRVITISVDTSKNQFSLKLTSSVTAADTAVYYCAYYDILGTGAFDINGQGTMTVTVSS 121

```

```

RESULT 5
US-10-309-762-138
Sequence 138. Application US/10309762
Publication No. US20040018158A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX 027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 138
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-138

```

[illegible]

```

RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYLIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

```

```
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-10
```

```
Query Match      83.0%; Score 509.5; DB 12; Length 123;
Best Local Similarity 82.2%; Pred. No. 1.2e-39;
Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;
```

```
OY 2 ESGPLVPSQTLSTLCTVSGSIRSGYMSWROPKGLWIGNTYHSGNTYNNPSL 61
    |||||
DB 6 ESGPLVPSQTLSTLCTVSGSIRSGYMSWIRQHPKGLWIGIYISGSTYNNPSL 65
    |||||
OY 62 KSRITMSVDTSKNHFSLRLTSVTADTAIVYYCARS-----DGYLDNMGGTLVTSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYYCARAGKYSGSYIDYWGQGTLVTVSS 123
    |||||
```

```
RESULT 7
US-10-309-762-11
```

```
Sequence 11, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudae, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-11
```

```
Query Match      82.7%; Score 507.5; DB 12; Length 125;
Best Local Similarity 81.7%; Pred. No. 1.8e-39;
Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;
```

```
OY 2 ESGPLVPSQTLSTLCTVSGSIRSGYMSWROPKGLWIGNTYHSGNTYNNPSL 61
    |||||
DB 6 ESGPLVPSQTLSTLCTVSGSIRSGYMSWIRQHPKGLWIGIYISGSTYNNPSL 65
    |||||
OY 62 KSRITMSVDTSKNHFSLRLTSVTADTAIVYYCARS-----DGYLDNMGGTLVTSS 114
    |||||
DB 66 KSRITISVDTSKNQFSLKLSSTVTAADTAIVYYCARFYIDELIYPPAFDLMGGMVTVSS 125
    |||||
```

```
RESULT 8
US-10-309-762-13
```

```
Sequence 13, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudae, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
```

```
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-13
```

```
Query Match      82.6%; Score 507; DB 12; Length 120;
Best Local Similarity 83.6%; Pred. No. 1.9e-39;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
```

```
OY 2 ESGPLVPSQTLSTLCTVSGSIRSGYMSWROPKGLWIGNTYHSGNTYNNPSL 61
    |||||
DB 6 ESGPLVPSQTLSTLCTVSGSIRSGYMSWIRQHPKGLWIGIYISGSTYNNPSL 65
    |||||
OY 62 KSRITMSVDTSKNHFSLRLTSVTADTAIVYYCARS-DGYLDNMGGTLVTSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYYCAR-DGYNVYFPLMGKGLTVTVSS 120
    |||||
```

```
RESULT 9
US-10-309-762-144
```

```
Sequence 144, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudae, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 144
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-144
```

```
Query Match      82.6%; Score 507; DB 12; Length 120;
Best Local Similarity 83.6%; Pred. No. 1.9e-39;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
```

```
OY 2 ESGPLVPSQTLSTLCTVSGSIRSGYMSWROPKGLWIGNTYHSGNTYNNPSL 61
    |||||
DB 6 ESGPLVPSQTLSTLCTVSGSIRSGYMSWIRQHPKGLWIGIYISGSTYNNPSL 65
    |||||
OY 62 KSRITMSVDTSKNHFSLRLTSVTADTAIVYYCARS-DGYLDNMGGTLVTSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYYCAR-DGYNVYFPLMGKGLTVTVSS 120
    |||||
```

```
RESULT 10
US-10-309-762-147
```

```
Sequence 147, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudae, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
```

```

1  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
2  TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
3  FILE REFERENCE: ABGENIX.027A
4  CURRENT APPLICATION NUMBER: US/10/309,762
5  CURRENT FILING DATE: 2002-12-02
6  PRIOR APPLICATION NUMBER: 60/337275
7  PRIOR FILING DATE: 2001-12-03
8  NUMBER OF SEQ ID NOS: 246
9  SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 147
11 LENGTH: 122
12 TYPE: PRT
13 ORGANISM: Homo sapiens
14 US-10-309-762-147

```

|                       |              |           |              |            |
|-----------------------|--------------|-----------|--------------|------------|
| Query Match           | 82.6%        | Score 507 | DB 12        | Length 122 |
| Best Local Similarity | 82.1%        | Pred. No. | 2e-39        |            |
| Matches 96            | Conservative | 8         | Mismatches 9 | Indels 4   |
|                       |              |           |              | Gaps 1     |

QY 2 ESQGLVKSQTLSLTCTVSGGSLRSGGYMSWVRPPGKGLWNIINIHSGNTYINPSL 61  
6 ESQGLVKSQTLSLTCTVSGGSLRSGGYMSWIRQHPKGLWNIQIYIYSSGRTYINPSL 65

62 KSRITMSVDTSKNPSLRITSVTAADTAVYCAR --- SGGYITDNGGQGLTVYSS 114  
66 KSRVTISVDTSKNGPSLRKTSVTAADTAVYCARYYDILGYGMDVMGQGTTVTVYSS 122

```

RESULT 11
US-09-972-656-80
: Sequence 80, Application US/09972656
: Publication No. US20030099647A1
: GENERAL INFORMATION:
: APPLICANT: Deshpande, Rajendra
: APPLICANT: Tsai, Mei-Mei
: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: FILE OF INVENTION: Neutralizing Activity
: FILE REFERENCE: A-799
: CURRENT APPLICATION NUMBER: US/09/972,656
: CURRENT FILING DATE: 2001-10-05
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 80
: LENGTH: 221
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-972-656-80

```

|    | Query Match           | 82.4%  | Score 506         | DB 11 | Length 221                      |
|----|-----------------------|--|-------------------|-------|---------------------------------|
|    | Best Local Similarity | 83.2%  | Pred. No. 4,4e-39 |       |                                 |
|    | Matches               | 94   | Conservative      | 7     | Mismatches 12; Indels 0; Gaps 0 |
| Qy | 2                     | ESGPELVKPSQTLSTCTVYSGGSIKSGGYWVWRQPKGKLEWIGNIYHSGNTYVPSL | 61                |       |                                 |
| Db | 6                     | ESGPVLKPSSETLSLTCVSGGSISSGGYSWIRQPKGLEWIGYIYHSGSTYVPSL   | 65                |       |                                 |
| Qy | 62                    | KSRIKMSVDTSKNHFSLRLTSTYAADTAVVYCARSDGYTLIDMGQGLTVSS      | 114               |       |                                 |
| Db | 66                    | KSRTVITSDRSGNQPSLKLSSVTAAADTAVVYCARQDQGFYDVGQGLTVYSS     | 118               |       |                                 |

RESULT 12  
US-10-309-762-151  
Sequence 151, Application US/10309762  
Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE INHIBITORS  
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN  
FILE REFERENCE: ABGENIX-027A

```

? CURRENT APPLICATION NUMBER: US/10/309,762
? CURRENT FILING DATE: 2002-12-02
? PRIOR APPLICATION NUMBER: 60/337275
? PRIOR FILING DATE: 2001-12-03
? NUMBER OF SEQ ID NOS: 246
? SOFTWARE: FastSeq for Windows Version 4.0.
? SEQ ID NO 151
? LENGTH: 121
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-309-762-151

```

|                       |       |              |         |            |    |        |     |
|-----------------------|-------|--------------|---------|------------|----|--------|-----|
| Query Match           | 82.3% | Score        | 505.5   | DB         | 12 | Length | 121 |
| Best Local Similarity | 82.8% | Pred. No.    | 2.7e-39 |            |    |        |     |
| Matches               | 96    | Conservative | 8       | Mismatches | 9  | Indels | 3   |
|                       |       |              |         |            |    | Gaps   | 1   |

Db 6 ES SGGLVLRPSQTSLTCTFVSGSGSISSGGYWSWIRQHPGKGLMEWIGYIYSGSGTYNPSL 65

62 KSRITMSVTSKHFPSLKRITSVIAADIAIYICAS--GGITLDMGGGLVIYSS 114  
66 KSRITISVDTSKQFSLKSLSVTAADIATVAYCARVLLMEWGYGMDVWGCGGTIVTVSS 121

```

RESULT 13
US-10-330-613-13
; Sequence 13, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENENT.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-13

```

[illegible]

```

RESULT 14
US-10-330-530-13
; Sequence 13, Application US/10330530
; Application No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENTX 031A
; CURRENT APPLICATION NUMBER: US/10/030,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ. ID NOS: 40
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 13

```





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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:46:18 ; Search time 34.3727 Seconds  
(without alignments)  
526.430 Million cell updates/sec

Title: US-10-027-725a-7

Perfect score: 609  
Sequence: 1 LESGGLVKAQTLISCAV.....RLDGYTLIDMGCTLVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq.19Jun03:\*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*

5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*

6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 609   | 100.0       | 114    | 23 | ABG30445    |
| 2          | 547   | 89.8        | 114    | 23 | ABG30447    |
| 3          | 546   | 89.7        | 114    | 23 | ABG30446    |
| 4          | 506.5 | 83.2        | 123    | 20 | AAW78433    |
| 5          | 506.5 | 83.2        | 123    | 23 | ABR97976    |
| 6          | 505   | 82.9        | 252    | 23 | ABP45983    |
| 7          | 502   | 82.4        | 123    | 22 | AA62745     |
| 8          | 500.5 | 82.2        | 251    | 24 | ABJ19829    |
| 9          | 499.5 | 82.0        | 120    | 22 | AA62775     |

|    |       |      |     |    |           |                    |
|----|-------|------|-----|----|-----------|--------------------|
| 10 | 499   | 81.9 | 473 | 22 | AA36206   | Human immune sys   |
| 11 | 498.5 | 81.9 | 253 | 23 | ABP45608  | Human Blys binding |
| 12 | 496   | 81.4 | 172 | 21 | AA93712   | The heavy chain of |
| 13 | 495.5 | 81.4 | 122 | 22 | AA62765   | Human HIV-1 monoc  |
| 14 | 493.5 | 81.0 | 129 | 23 | AAU81275  | Human tdkc antibod |
| 15 | 490   | 80.5 | 126 | 21 | AA30584   | A human variable h |
| 16 | 490   | 80.5 | 126 | 23 | ABP45970  | Anti-idiotypic VH  |
| 17 | 490   | 80.5 | 130 | 23 | AAU81273  | Human tdkc antibod |
| 18 | 490   | 80.5 | 251 | 23 | ABG80712  | Amyloid peptide co |
| 19 | 490   | 80.5 | 254 | 23 | ABG80713  | Amyloid peptide co |
| 20 | 490   | 80.5 | 263 | 23 | ABG80714  | Human IgG/factor x |
| 21 | 489   | 80.3 | 118 | 20 | AAU81276  | Humanised LM609 an |
| 22 | 483.5 | 79.4 | 129 | 23 | AAU81276  | Human tdkc antibod |
| 23 | 482   | 79.1 | 256 | 23 | ABP45596  | Human Blys binding |
| 24 | 482   | 79.1 | 487 | 22 | ABP90607  | Human secreted pro |
| 25 | 482   | 79.1 | 487 | 23 | ABG65445  | Human albumin fusi |
| 26 | 481   | 79.0 | 246 | 21 | AAV15126  | Anti-murine CTLA-4 |
| 27 | 479   | 78.7 | 118 | 20 | AAV06386  | Humanised LM609 an |
| 28 | 477   | 78.3 | 118 | 20 | AAV06383  | Humanised LM609 an |
| 29 | 474   | 77.8 | 252 | 23 | ABP45318  | Human Blys binding |
| 30 | 474   | 77.8 | 256 | 23 | ABP45734  | Human Blys binding |
| 31 | 473   | 77.7 | 229 | 21 | ABG30593  | Human albumin fusi |
| 32 | 471.5 | 77.4 | 119 | 14 | AA30143   | Variable and first |
| 33 | 471.5 | 77.4 | 119 | 18 | AAW27554  | Mab GAH variable r |
| 34 | 471.5 | 77.4 | 119 | 24 | ABP98683  | Human Ab heavy cha |
| 35 | 471.5 | 77.4 | 119 | 24 | ABP98691  | Human GAH antibody |
| 36 | 471.5 | 77.4 | 119 | 24 | ABJ18676  | Human GAH antibody |
| 37 | 471   | 77.3 | 250 | 23 | ABP45537  | Antibody library r |
| 38 | 470.5 | 77.3 | 127 | 22 | AAAG80217 | Human Blys binding |
| 39 | 468   | 76.8 | 120 | 20 | AAW90287  | Human autoantibody |
| 40 | 465.5 | 76.4 | 117 | 21 | AAV44615  | Human anti-GR1b/I  |
| 41 | 465   | 76.4 | 248 | 23 | ABP45349  | Human antibody clo |
| 42 | 464.5 | 76.3 | 251 | 23 | ABP44979  | Human Blys binding |
| 43 | 464   | 76.2 | 117 | 22 | AAU02540  | Human Blys binding |
| 44 | 463   | 76.0 | 118 | 20 | AAV06384  | Anti-adipocyte mon |
| 45 | 463   | 76.0 | 126 | 23 | ABG32888  | Humanised LM609 an |

## ALIGNMENTS

|          |             |  |
|----------|-------------|--|
| RESULT 1 | ABG30445    | standard; Protein, 114 AA.                                 |
| ID       | ABG30445    |  |
| XX       | ABG30445;   |  |
| AC       | 21-OCT-2002 | (first entry)  |
| XX       |             |  |
| DT       |             |  |
| XX       |             |  |
| DE       |             | Human Ige Fab clone 94 heavy chain protein.                |
| XX       |             |  |
| KW       |             | Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2; |
| KW       |             | timothy grass pollen allergen; passive immunotherapy.      |
| XX       |             |  |
| OS       |             | Homo sapiens.  |
| XX       |             |  |
| FH       | Key         | Location/Qualifiers  |
| FT       | Region      | 1..26  |
| FT       |             | /note= "FR1 region"  |
| FT       | Region      | 27..33   |
| FT       |             | /note= "CDR1 region"                                       |
| FT       | Region      | 34..47   |
| FT       |             | /note= "FR2 region"  |
| FT       | Region      | 48..63   |
| FT       |             | /note= "CDR2 protein"                                      |
| FT       | Region      | 64..95   |
| FT       |             | /note= "FR3 region"  |
| FT       | Region      | 96..103  |
| FT       |             | /note= "CDR2 region"                                       |
| FT       | Region      | 104..114   |
| FT       |             | /note= "FR4 region"  |
| XX       |             |  |
| PN       |             | WO200253595-A1.  |

```

XX 11-JUL-2002.
PD 27-DEC-2001; 2001WO-SE02908.
PF 29-DEC-2000; 2000SE-0004892.
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX Flicker S, Steinberger P, Kraft D, Valenta R;
PI MPI; 2002-583604/62.
DR N-PSDB; ABK89637.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for
PT environmental allergen detection -
XX
XX Disclosure; Page 36; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human IgE Fabs and methods for their use. The proteins
XX of the invention may have antiallergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergic patient's
XX IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).
XX The group 2 allergen-specific Fabs of the invention may be useful for
XX environmental allergen detection and for standardisation of allergen
XX extracts. The Fabs - or a vaccine against a type I allergy is useful for
XX passive immunotherapy of type I allergy. It is also useful for
XX diagnosing a type I allergy. The allergen-specific Fabs of the invention
XX are useful for inter alia, diagnosis, therapy and prevention of type
XX I allergy. They are also useful for identification of group 2
XX allergen-containing pollen and may be used for blocking the binding of
XX grass pollen allergic patients IgE antibodies to Phi p 2. The present
XX sequence represents the human IgG fab, clone 94 heavy chain protein of
XX the invention.
XX
XX Sequence 114 AA;
SQ
Query Match 100.0%; Score 609; DB 23; Length 114;
Best Local Similarity 100.0%; Pred. No. 4,8e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKSGPGLVPAQTLISLSCAVSGSIRGGYVSWIRHPGKLEWIGYIYHSGNTYVNS 60
DB 1 LKSGPGLVPAQTLISLSCAVSGSIRGGYVSWIRHPGKLEWIGYIYHSGNTYVNS 60
QY 61 LKSRIMSVDTSENKFSRLNSVTAAADTVAVYYCARLDGYTLDIWGQGLVTYVSS 114
DB 61 LKSRIMSVDTSENKFSRLNSVTAAADTVAVYYCARLDGYTLDIWGQGLVTYVSS 114
RESULT 2
ABG30447 standard; Protein; 114 AA.
XX
XX ABG30447;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Human IgE Fab clone 100 heavy chain protein.
DE
XX
XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 1..26
FT /note= "FRI region"
FT 27..33
FT Region
FT /note= "CDRI region"

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FT Region 34..47
FT /note= "FR2 region"
FT 48..63
FT Region
FT /note= "CDR2 protein"
FT 64..95
FT Region
FT /note= "FR3 region"
FT 96..103
FT Region
FT /note= "CDR2 region"
FT 104..114
FT /note= "FR4 region"
XX
XX WO200253595-A1.
XX
XX 11-JUL-2002.
PD
XX
XX 27-DEC-2001; 2001WO-SE02908.
PF
XX
XX 29-DEC-2000; 2000SE-0004892.
XX
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
PI MPI; 2002-583604/62.
DR N-PSDB; ABK89639.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for
PT environmental allergen detection -
XX
XX Disclosure; Page 38; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human IgE Fabs and methods for their use. The proteins
XX of the invention may have antiallergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergic patient's
XX IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).
XX The group 2 allergen-specific Fabs of the invention may be useful for
XX environmental allergen detection and for standardisation of allergen
XX extracts. The Fabs - or a vaccine against a type I allergy is useful for
XX passive immunotherapy of type I allergy. It is also useful for
XX diagnosing a type I allergy. The allergen-specific Fabs of the invention
XX are useful for inter alia, diagnosis, therapy and prevention of type
XX I allergy. They are also useful for identification of group 2
XX allergen-containing pollen and may be used for blocking the binding of
XX grass pollen allergic patients IgE antibodies to Phi p 2. The present
XX sequence represents the human IgG fab, clone 100 heavy chain protein of
XX the invention.
XX
XX Sequence 114 AA;
SQ
Query Match 89.8%; Score 547; DB 23; Length 114;
Best Local Similarity 89.5%; Pred. No. 3,4e-44;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 LKSGPGLVPAQTLISLSCAVSGSIRGGYVSWIRHPGKLEWIGYIYHSGNTYVNS 60
DB 1 LKSGPGLVPAQTLISLSCAVSGSIRGGYVSWIRHPGKLEWIGYIYHSGNTYVNS 60
QY 61 LKSRIMSVDTSENKFSRLNSVTAAADTVAVYYCARLDGYTLDIWGQGLVTYVSS 114
DB 61 LKSRIMSVDTSENKFSRLNSVTAAADTVAVYYCARLDGYTLDIWGQGLVTYVSS 114
RESULT 3
ABG30446 standard; Protein; 114 AA.
XX
XX ABG30446;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX

```

DE Human Ige Fab clone 60 heavy chain protein.  
 XX Human, fab; anti allergic; vaccine; grass pollen; Phi p 2;  
 KM timothy grass pollen allergen; passive immunotherapy.  
 XX Homo sapiens.  
 XX Location/Qualifiers  
 FT Key 1..26  
 FT Region /note= "FR1 region"  
 FT Region 27..33  
 FT Region /note= "CDR1 region"  
 FT Region 34..47  
 FT Region /note= "FR2 region"  
 FT Region 48..63  
 FT Region /note= "CDR2 protein"  
 FT Region 64..95  
 FT Region /note= "FR3 region"  
 FT Region 96..103  
 FT Region /note= "CDR2 region"  
 FT Region 104..114  
 FT Region /note= "FR4 region"  
 XX MO200253595-A1.  
 XX 11-JUL-2002.  
 XX 27-DEC-2001; 2001MO-SE02908.  
 XX 29-DEC-2000; 2000SE-0004892.  
 XX (PHAA ) PHARMACIA DIAGNOSTICS AB.  
 XX Flicker S, Steibberger P, Kraft D, Valenta R;  
 XX WPI: 2002-583604/62.  
 XX N-P8DB; ABR89638.  
 XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human Ige Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for  
 PT environmental allergen detection -  
 XX Disclosure: Page 37; 45pp; English.  
 XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human Ige Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's  
 CC Ige antibodies to Phi p 2 (a major timothy grass pollen allergen).  
 CC The group 2 allergen-specific fabs of the invention may be useful for  
 CC environmental allergen detection and for standardisation of allergen  
 CC extracts. The fabs - or a vaccine against a type I allergy is useful for  
 CC passive immunotherapy of type I allergy, it is also useful for  
 CC diagnosing a type I allergy. The allergen-specific fabs of the invention  
 CC are useful for inter alia, diagnosis, therapy and prevention of type  
 CC I allergy. They are also useful for identification of group 2  
 CC allergen-containing pollen and may be used for blocking the binding of  
 CC grass pollen allergic patients Ige antibodies to Phi p 2. The present  
 CC sequence represents the human Ige fab, clone 60 heavy chain protein of  
 CC the invention.  
 XX Sequence 114 AA;  
 SO  
 Query Match 89.7%; Score 546; DB 23; Length 114;  
 Best Local Similarity 89.5%; Pred. No. 4.2e-44;  
 Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 LESGGLVPAQTSLSCAVSGSIRSGGYWSWIRHPGKGLMIGIYHSGNTYVPS 60  
 DB 1 LESGGLVPAQTSLSCAVSGSIRSGGYWSWIRHPGKGLMIGIYHSGNTYVPS 60  
 QY 61 LKSRIMSVDTSENKFSRLNSVTADTAVYYCARLDLDDYDYGSGASDYGQGLTVTVSS 114  
 DB 61 LKSRIMSVDTSENKFSRLNSVTADTAVYYCARLDLDDYDYGSGASDYGQGLTVTVSS 114

DB  
 |||||  
 61 LKSRIMSVDTSENKFSRLNSVTADTAVYYCARLDLDDYDYGSGASDYGQGLTVTVSS 114  
 RESULT 4  
 ID AAM78433 standard; Protein; 123 AA.  
 XX AAM78433;  
 AC AAM78433;  
 DT 11-MAY-1999 (first entry)  
 DE Antibody heavy chain targeted to obr clone 26.  
 XX Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;  
 KM diagnosis; cancer; primer; PCR; amplification; diagnostic.  
 XX Synthetic.  
 OS WO9850431-A2.  
 XX WO9850431-A2.  
 XX 12-NOV-1998.  
 XX 30-APR-1998; 98WO-US08762.  
 XX 24-JUN-1997; 97US-0050661.  
 XX 02-MAY-1997; 97US-0850058.  
 XX (GETH ) GENENTECH INC.  
 XX Archthon R, Carter PJ, Merchant AM, Presta LG;  
 PI WPI: 1999-070091/06.  
 XX Selective preparation of multispecific antibodies - with  
 PT heteromultimeric heavy chain and common light chain components,  
 PT useful for, e.g. in vivo diagnosis of cancer  
 XX Example 4; Fig 5; 69pp; English.  
 XX This sequence represents the heavy chain variable region for an antibody  
 CC that binds to the obr clone 26 protein. The sequence encoding the chain  
 CC is generated by a new method for preparing a multispecific Ab comprising  
 CC a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP  
 CC comprises a multimerisation domain (MD) forming an interface positioned  
 CC to interact with an interface of a MD of the extra PP; and (ii) the first  
 CC and extra PPs each have a binding domain, which comprises a heavy chain  
 CC and a light chain, where the variable light chains of the first and extra  
 CC PPs comprise a common sequence. The method comprises: (a) culturing a  
 CC host cell comprising nucleic acid encoding the first PP and extra PP, and  
 CC the variable light chain, such that the nucleic acid is expressed; and  
 CC (b) recovering the multispecific Ab from the culture. The method prepares  
 CC heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins  
 CC and Ab-immunoadhesin chimeras. The method allows for the enhanced  
 CC formation of the desired heteromultimer relative to the undesired  
 CC heteromultimers and homomultimers. The Abs can be used in immunoassays  
 CC and for the in vitro or in vivo diagnosis of various diseases, such as  
 CC cancer.  
 XX Sequence 123 AA;  
 SO  
 Query Match 83.2%; Score 506.5; DB 20; Length 123;  
 Best Local Similarity 79.0%; Pred. No. 2.5e-40;  
 Matches 94; Conservative 12; Mismatches 8; Indels 5; Gaps 1;  
 QY 1 LESGGLVPAQTSLSCAVSGSIRSGGYWSWIRHPGKGLMIGIYHSGNTYVPS 60  
 DB 5 VESGGLVPAQTSLSCAVSGSIRSGGYWSWIRHPGKGLMIGIYHSGNTYVPS 64  
 QY 61 LKSRIMSVDTSENKFSRLNSVTADTAVYYCARLDLDDYDYGSGASDYGQGLTVTVSS 114  
 DB 65 LKSRIMSVDTSENKFSRLNSVTADTAVYYCARLDLDDYDYGSGASDYGQGLTVTVSS 123

## RESULT 5

ID ABB97976 standard; Protein; 123 AA.

XX ABB97976;

DT 06-SEP-2002 (first entry)

XX Heavy chain variable region from antibody obr.26.

XX Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;  
KM antiviral; vaccine; tumour.

XX Synthetic.

XX US2002062010-A1.

XX 23-MAY-2002.

XX 23-MAY-2001; 2001US-0863693.

XX 02-MAY-1997; 97US-046816P.

XX 30-APR-1998; 98US-0070166.

XX (GENTH ) GENENTECH INC.

XX Arathoon WR, Carter PJ, Merchant AM, Presta LG;

XX MPI; 2002-499676/53.

PT New multispecific antibodies having heteromultimeric and common  
PT components are useful to direct treatment to a target site such as a  
PT tumour cell, cell surface receptor or clon, as a vaccine adjuvant and to  
PT treat infectious disease

PS Example 4; Fig 5; 36pp; English.

XX The invention relates to a new multispecific antibody, comprising at  
CC least two polypeptides (PP1 and PP2) which meet at a multiface, where PP1  
CC has a multimerisation domain forming an interface positioned to interact  
CC with an interface of a multimerisation domain of PP2, and both  
CC polypeptides each comprise a binding domain consisting a heavy chain and  
CC a variable light chain, where the light chain has a sequence common to  
CC both polypeptides. Heteromultimers of the inventions include bispecific  
CC antibodies, bispecific immunoadhesins and antibody-immunoadhesin  
CC chimeras. The activity of antibodies of the invention may be described  
CC as, cytostatic, antibacterial and antiviral. The heteromultimer  
CC can be used for redirected cytotoxicity, for example to kill tumour  
CC cells, as a vaccine adjuvant, for delivering thrombolytic agents to  
CC clots, for converting enzyme activated prodrugs at a target site such as  
CC a tumour, for treating infectious diseases, for targeting immune  
CC complexes to cell surface receptors or for delivering immunotoxins to  
CC tumour cells. The current sequence represents the heavy chain variable  
CC region from antibody obr.26 used in the construction of bispecific  
CC antibodies.

XX Sequence 123 AA;

SQ Query Match 83.2%; Score 506.5; DB 23; Length 123;

Best Local Similarity 79.0%; Pred. No.2,5e-40;

Matches 94; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

QY 1 LBSGPGLVKPAQTLISLCAVSGSISGSGYWMIRHPEKGLWIGIYIHSGNTYNNPS 60

DB 5 VESGPGVLVKSQTLISLCTVSGSGISGSGYWMIRHPEKGLWIGIYIYSGSTYNNPS 64

QY 61 LKSRIMSVDTSENKPSLRINSVTAAADTAVYCARLD-----GTTLDIMGCGTLTVSS 114

DB 65 LKSRVITSVDTSENKPSLRINSVTAAADTAVYCARLDLEDYSGSGASDYMGGGTLTVSS 123

## RESULT 6

## ABP45983

ID ABP45983 standard; Protein; 252 AA.

XX AC ABP45983;

DT 19-AUG-2002 (first entry)

XX Human B.Lys binding scFv SEQ ID 1994.

XX B.Lys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JUN-2002.

XX 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

XX 17-OCT-2000; 2000US-240816P.

XX 16-MAR-2001; 2001US-276248P.

XX 21-MAR-2001; 2001US-277379P.

XX 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX MPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for

XX the diagnosis and treatment of cancers and immune disorders -

XX Claim 1; Page 2779-2780; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (BLys) polypeptides. BLys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of BLys. The antibodies bind to BLys  
CC and so may be used to detect and quantitate the presence of BLys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of BLys. They may also be  
CC administered to treat diseases associated with aberrant BLys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.

XX Sequence 252 AA;

SQ Query Match 82.9%; Score 505; DB 23; Length 252;

Best Local Similarity 78.2%; Pred. No.7,5e-40;

Matches 93; Conservative 12; Mismatches 8; Indels 6; Gaps 1;

QY 2 ESGPGVLKPAQTLISLCAVSGSISGSGYWMIRHPEKGLWIGIYIHSGNTYNNPSL 61

DB 6 ESGPGVLKPSQTLISLCTVSGSGISGSGYWMIRHPEKGLWIGIYIHSSTYNNPSL 65

QY 62 KSRIMSVDTSENKPSLRINSVTAAADTAVYCARL-----DGYTLDIMGCGTLTVSS 114

DB 66 KSRVSVSVDTSENKPSLRINSVTAAADTAVYCARLPDADYGDYGGGTLTVSS 124

RESULT 7  
AAB62745  
ID AAB62745 standard; Protein; 123 AA.  
XX  
AC AAB62745;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Human HIV-1 monoclonal antibody SEQ ID NO: 44.  
XX  
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
KW envelope glycoprotein; gp120; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200100678-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000MO-US17327.  
XX  
PR 30-JUN-1999; 99US-0141701.  
XX  
PA (US) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Watkins BA, Reitz MS;  
XX  
DR WPI; 2001-112438/12.  
XX  
DR N-PSDB; AAF29046.  
XX  
PT Novel human monoclonal antibody immunoreactive with human  
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
PT in biological sample and providing passive immunotherapy to HIV-1  
XX infected mammal -  
XX  
PS Claim 1; Page 50; 81pp; English.  
XX  
CC The present invention provides the protein and coding sequences for the  
CC variable regions of human monoclonal antibodies which are immunoreactive  
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
CC These can be used in diagnosis and therapy of HIV-1 infection.  
XX  
SQ Sequence 123 AA;  
XX  
Query Match 82.4%; Score 502; DB 22; Length 123;  
Best Local Similarity 79.5%; Pred. No. 6.6e-40;  
Matches 93; Conservative 11; Mismatches 9; Indels 4; Gaps 1;  
XX  
QY 2 ESGPGLVPAQTLISCAVSGSIRSGYMSWIRHFGKLEWIGYIHSGNTYNSL 61  
DB 7 ESGPGLVPAQTLISCAVSGSIRSGYMSWIRHFGKLEWIGYIHSGNTYNSL 66  
QY 62 KSRIAMSVDTSENKPSLRLNSTADTAVYVCARL---DGYTLIDWGCTLVVSS 114  
DB 67 KSRIAMSVDTSENKPSLRLNSTADTAVYVCARL---DGYTLIDWGCTLVVSS 123  
XX  
RESULT 8  
AAB19829  
ID AAB19829 standard; Protein; 251 AA.  
XX  
AC AAB19829;  
XX  
DT 10-APR-2003 (first entry)  
XX  
DE Human VEGF-2 related protein SEQ ID No 75.  
XX  
KW Cytostatic; cardiant; cardiovascular; antiinflammatory; antithematic;  
KW antitachytic; antidiabetic; ophthalmological; antiallergic;  
KW immunosuppressive; dermatological; antiporiatic; vulnary; antibody;  
KW CDR region; VH domain; VL domain; immunospecific; VEGF-2; cancer;  
XX

KW proliferative disorder; cardiovascular disorder; arrhythmia;  
KW cerebrovascular disorder; cerebral anoxia; inflammatory disease;  
KW infectious disease; autoimmune disease; rheumatoid arthritis;  
KW Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis;  
KW angiogenesis; wound healing; vascular tissue repair; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200283704-A1.  
XX  
PD 24-OCT-2002.  
XX  
PF 12-APR-2002; 2002WO-US11474.  
XX  
PR 13-APR-2001; 2001US-283385P.  
XX  
PR 24-JAN-2002; 2002US-350366P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Albert VR, Ruben SM, Wager RE;  
XX  
DR WPI; 2003-092991/08.  
XX  
PT New isolated polynucleotide encoding an antibody which inhibits a  
PT VEGF-2 polypeptide, useful for diagnosing, treating or preventing  
PT diseases associated with aberrant VEGF-2 expression or function, e.g.  
PT cancer or inflammation -  
XX  
PS Disclosure; Page 385-386; 425pp; English.  
XX  
CC The invention relates to an isolated polynucleotide encoding a first  
CC antibody at least 95-100% identical to a second antibody comprising an  
CC amino acid sequence selected from at least one, two or three CDR  
CC region(s) of a VH or VL domain where the first antibody  
CC immunospecifically inhibits a VEGF-2 polypeptide. The isolated  
CC polynucleotide is useful in diagnosing, treating, preventing, prognosing,  
CC ameliorating or monitoring diseases associated with aberrant VEGF-2 or  
CC VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function,  
CC such as cancer and other proliferative disorders, cardiovascular  
CC disorders (arrhythmias), cerebrovascular disorders (e.g. cerebral  
CC anoxia), inflammatory diseases, infectious diseases, autoimmune diseases  
CC (e.g. Rheumatoid arthritis, Systemic Lupus Erythematosus, allergies),  
CC diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and  
CC antibodies may also be used to stimulate angiogenesis, wound healing, and  
CC promoting vascular tissue repair. The polynucleotide and polypeptide may  
CC also be used for in vitro purposes related to scientific research,  
CC synthesis of DNA and manufacture of DNA vectors, and for the production  
CC of diagnostics and therapeutics to treat human diseases. This sequence  
CC represents a human VEGF-2 related protein of the invention.  
XX  
SQ Sequence 251 AA;  
XX  
Query Match 82.2%; Score 500.5; DB 24; Length 251;  
Best Local Similarity 79.7%; Pred. No. 2e-39;  
Matches 94; Conservative 13; Mismatches 6; Indels 5; Gaps 2;  
XX  
QY 2 ESGPGLVPAQTLISCAVSGSIRSGYMSWIRHFGKLEWIGYIHSGNTYNSL 61  
DB 6 ESGPGLVPAQTLISCAVSGSIRSGYMSWIRHFGKLEWIGYIHSGNTYNSL 65  
QY 62 KSRIAMSVDTSENKPSLRLNSTADTAVYVCAR---LDGYT---LDWGCTLVVSS 114  
DB 66 KSRIAMSVDTSENKPSLRLNSTADTAVYVCAR---LDGYT---LDWGCTLVVSS 123  
XX  
RESULT 9  
AAB62775  
ID AAB62775 standard; Protein; 120 AA.  
XX  
AC AAB62775;  
XX  
DT 03-APR-2001 (first entry)  
XX

DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.  
XX  
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
KM envelope glycoprotein; gp120; diagnosis.  
XX  
XX Homo sapiens.  
XX  
XX WO200100678-A1.  
XX  
XX 04-JUN-2001.  
XX  
XX 23-JUN-2000; 2000WO-US17327.  
XX  
XX 30-JUN-1999; 99US-0141701.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Watkins BA, Reitz MS;  
XX  
XX WPI: 2001-112438/12.  
XX  
XX N-PSDB; AAF29076.  
XX  
XX Novel human monoclonal antibody immunoreactive with human  
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
PT in biological sample and providing passive immunotherapy to HIV-1  
PT infected mammal -  
XX  
XX Claim 1; Page 69; 81pp; English.  
XX  
XX The present invention provides the protein and coding sequences for the  
CC variable regions of human monoclonal antibodies which are immunoreactive  
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
CC These can be used in diagnosis and therapy of HIV-1 infection.  
XX  
XX Sequence 120 AA;  
SQ  
Query Match 82.0%; Score 499.5; DB 22; Length 120;  
Best Local Similarity 81.0%; Pred. No. 1.1e-39;  
Matches 94; Conservative 12; Mismatches 5; Indels 5; Gaps 2;  
QY 2 ESGPGLVKKPAQTLSLSCAVSGSIRSGYWSMIRQPKGLEWIGYIHSGNTYNPSTL 61  
DB 7 ESGPGLVKKPQSTLSLCTVSGSISGQYWSMIRQPKGLEWIGYIYSGSTYNPSTL 66  
QY 62 KSRIMSVDTSEKPSLRINSVTAAADTAVYYCAR---LDGYTLDINGCGTLTVSS 114  
DB 67 KSRVTISVDTSKNQPSLKLSTVTAADTAVYYCARGVVDMF--DPWGQGTLLTVSS 120  
RESULT 10  
AAB36206  
ID AAB36206 standard; protein; 473 AA.  
XX  
XX AAB36206;  
AC  
XX  
XX 15-FEB-2001 (first entry)  
DT  
XX  
XX Human immune system associated protein HISAP-4.  
DE  
XX  
XX Human; immune system associated protein; HISAP-4; immune disorder;  
KM infection; autoimmune disease; cancer.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US6135941-A.  
XX  
XX 24-OCT-2000.  
XX  
XX 27-MAR-1998; 98US-0049672.  
XX  
XX 27-MAR-1998; 98US-0049672.  
XX  
XX (INCY-) INCYTE PHARM INC.  
PA

XX  
XX Tang YT, Yue H, Iai P, Corley NC, Guegler KJ, Baughn MR;  
PI Hillman JL, Au-Young J;  
XX  
XX WPI: 2001-030926/04.  
XX  
XX N-PSDB; AAC65522.  
XX  
XX New human immune system associated proteins (HISAP) and polynucleotides  
PT encoding the HISAP, useful for diagnosing, treating or preventing  
PT immune or cell proliferative disorders or infections -  
XX  
XX Claim 1; Column 53-56; 54pp; English.  
XX  
XX The present invention provides the coding and protein sequences for a  
CC number of human immune system associated proteins (HISAPs). These can be  
CC used in the diagnosis and treatment of various autoimmune disorders,  
CC infections and cell proliferation diseases. The diseases include AIDS,  
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
CC erythematosus, arteriosclerosis, cirrhosis and cancer.  
XX  
XX Sequence 473 AA;  
SQ  
Query Match 81.9%; Score 499; DB 22; Length 473;  
Best Local Similarity 78.2%; Pred. No. 5.5e-39;  
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;  
QY 2 ESGPGLVKKPAQTLSLSCAVSGSIRSGYWSMIRQPKGLEWIGYIHSGNTYNPSTL 61  
DB 25 ESGPGLVKKPSESTLSLCTVSGSISGQYWSMIRQPKGLEWIGYIYSGSTYNPSTL 84  
QY 62 KSRIMSVDTSEKPSLRINSVTAAADTAVYYCARLD-----GYTLDINGCGTLTVSS 114  
DB 85 KSRVTISVDTSKNQPSLKLSTVTAADTAVYYCARDVCGRGANTGVDMVGQGTLLTVSS 143  
RESULT 11  
AAB45608  
ID AAB45608 standard; Protein; 253 AA.  
XX  
XX AAB45608;  
AC  
XX  
XX 19-AUG-2002 (first entry)  
DT  
XX  
XX Human Blys binding scFv SEQ ID 1619.  
DE  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US19110.  
XX  
XX 16-JUN-2000; 2000US-212210P.  
XX  
XX 17-OCT-2000; 2000US-240816P.  
XX  
XX 16-MAR-2001; 2001US-276248P.  
XX  
XX 21-MAR-2001; 2001US-277379P.  
XX  
XX 25-MAY-2001; 2001US-293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX (CAMA-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX



DR MPI; 2002-11479/15.  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for  
PT the diagnosis and treatment of cancers and immune disorders -  
XX  
XX Claim 1; Page 2335-2336; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumor necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antineoplastic, and anti-AIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
SQ Sequence 253 AA;  
XX  
Query Match 81.9%; Score 498.5; DB 23; Length 253;  
Best Local Similarity 77.9%; Pred. No. 3.1e-39;  
Matches 95; Conservative 12; Mismatches 6; Indels 9; Gaps 3;  
XX  
QY 2 ESGPLVLRPAQTLISCAVSGSIRSGGYWMIROHPKGLWIGYIHGNTYYPNL 61  
DB 6 ESGPLVLRPAQTLISCAVSGSIRSGGYWMIROHPKGLWIGYIHGNTYYPNL 65  
QY 62 KSRIAMSVTSENKSLRLNSTAADTAAYYCAR----LDG--YT--LDINGGCTLVTV 112  
DB 66 KSRVITSDTSKNQPSLKLSTVTAADTAAYYCVRSYTDILTRPTDADFMKGTLTV 125  
QY 113 SS 114  
DB 126 SS 127  
XX  
RESULT 12  
AA93713  
ID AA93713 standard; Protein; 172 AA.  
AC AA93713;  
XX  
DT 03-OCT-2000 (first entry)  
XX  
DE The heavy chain of immunoglobulin clone 2.1.3.  
XX  
KM Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
KM hyperimmune disorder; autoimmune disease; diabetes; graft rejection;  
KM proliferative disorder; cancer; immunodeficient disorder.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200037504-A2.  
XX PN  
XX 29-JUN-2000.  
XX PD  
XX 23-DEC-1999; 99WO-US30895.  
XX PF  
XX 23-DEC-1998; 98US-0113647.  
XX PR  
XX (PFI2) PFIZER INC.  
XX PA (ABGE-) ABGENIX INC.  
XX  
XX Hanson DC, Neveu MJ, Mueller BE, Hanke JH, Gilman SC, Davis CG;  
PI Corvajan JR;

XX  
XX MPI; 2000-442647/38.  
DR N-PSDB; AAA46876.  
XX  
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen  
PT (CTLA-4) containing specified heavy and light chain sequences, useful  
PT for treating, e.g. immune disorders -  
XX  
XX Claim 2; Fig 1G; 157pp; English.  
XX  
XX The present sequence represents a heavy chain of an antibody of the  
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen  
CC (CTLA-4). Antibodies of the invention are composed of a heavy chain  
CC variable region, comprising a modified contiguous sequence from a  
CC FRI-FRI sequence encoded by a human VH3-33 family gene. The  
CC modifications are contained in CDR1, CDR2 and/or framework regions.  
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the  
CC immune system to treat hyperimmunity disorders (e.g. autoimmune  
CC disease, diabetes and graft rejection) and proliferative disorders  
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate  
CC immune system to up-regulate immunodeficient disorders.  
XX  
SQ Sequence 172 AA;  
XX  
Query Match 81.4%; Score 496; DB 21; Length 172;  
Best Local Similarity 79.8%; Pred. No. 3.5e-39;  
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;  
XX  
QY 3 SGPLVLRPAQTLISCAVSGSIRSGGYWMIROHPKGLWIGYIHGNTYYPNL 62  
DB 1 SGPLVLRPAQTLISCAVSGSIRSGGYWMIROHPKGLWIGYIHGNTYYPNL 60  
QY 63 SRIMASVTSNENKSLRLNSTAADTAAYYCARLDG--YTLDINGGCTLVTVSS 114  
DB 61 SRVITSDTSKNQPSLKLSTVTAADTAAYYCARSDGYGIDVWGQGTTVVSS 114  
XX  
RESULT 13  
AAB62765  
ID AAB62765 standard; Protein; 122 AA.  
AC AAB62765;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Human HIV-1 monoclonal antibody SEQ ID NO: 64.  
XX  
KM Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
KM envelope glycoprotein; gp120; diagnosis.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200100678-A1.  
XX PN  
XX 04-JAN-2001.  
XX PD  
XX 23-JUN-2000; 2000WO-US17327.  
XX PF  
XX 30-JUN-1999; 99US-014701.  
XX PR  
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Watkins BA, Reitz MS;  
XX PI  
XX MPI; 2001-112438/12.  
XX DR N-PSDB; AAF29066.  
XX  
XX Novel human monoclonal antibody immunoreactive with human  
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
PT in biological sample and providing passive immunotherapy to HIV-1  
PT infected mammal -  
XX  
XX Claim 1; Page 63; 81pp; English.

XX The present invention provides the protein and coding sequences for the  
 CC variable regions of human monoclonal antibodies which are immunoreactive  
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
 CC These can be used in diagnosis and therapy of HIV-1 infection.  
 CC  
 XX Sequence 122 AA;  
 SQ  
 Query Match 81.4%; Score 495.5; DB 22; Length 122;  
 Best Local Similarity 80.2%; Pred. No. 2,7e-39;  
 Matches 93; Conservative 11; Mismatches 9; Indels 3; Gaps 1;  
 QY 2 ESGPGVLPACQTLSTSCAVSGGSIIRSGGYWMIHQHKGLEWIGYIYHSGNTYYPSTL 61  
 DB 7 ESGPGVLPKPSQTLSTCTVSGGSIIRSGGYWMIHQHKGLEWIGYIYHSGNTYYPSTL 66  
 QY 62 KSRIAMSVDTSENKFSRLNSVTADTAVYYCAR---LDGYTLDIWGOGTLVTVSS 114  
 DB 67 KSRVTISVDTSKNPSLKLSVTADTAVYYCARDLMLRDSGTGLCYWGRGTLVTVSS 122  
 RESULT 14  
 ID AAB31275  
 AAU81275 standard; Protein; 129 AA.  
 AC AAU81275;  
 DT 09-APR-2002 (first entry)  
 XX Human tcrK antibody heavy chain variable region #3.  
 DE  
 XX Human; mouse; anti-tcrK agonist monoclonal antibody; tcrK; antibody;  
 KM tcrK; tcrB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;  
 KM peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;  
 KM large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;  
 KM nerve cell injury; blood cell disorder; leukopenia; eosinopenia; wound;  
 KM basopenia; lymphopenia; monocytopenia; neutropenia; cancer; ulcer;  
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;  
 KM sickle cell disease; cardiac ischaemia; cerebrovascular disorder;  
 KM cellular degeneration; gene therapy.  
 KM  
 OS Homo sapiens.  
 XX  
 PN WO200198361-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 22-JUN-2001; 2001WO-US20153.  
 XX  
 PR 22-JUN-2000; 2000US-213141P.  
 PR 05-OCT-2000; 2000US-238319P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Devaux B, Hongo JS, Presta LG, Shelton DL;  
 XX  
 DR WPI, 2002-130790/17.  
 DR N-PSDB; ABR24410.  
 XX  
 PT Novel anti-tcrK agonist monoclonal antibody useful for treating  
 PT neurodegenerative disease, shows no significant cross-reactivity with  
 PT tcrK/tcrB, and recognizes epitope in domain 5 of tcrK -  
 XX  
 PS Example 1; Fig 9; 121pp; English.  
 XX  
 CC The invention relates to an anti-tcrK agonist monoclonal antibody which  
 CC shows no significant cross-reactivity with tcrK or tcrB, and recognizes  
 CC an epitope in domain 5 of tcrK. The antibodies of the invention are  
 CC effective in the treatment of cisplatin- or pyridoxine-induced  
 CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre  
 CC sensory neuropathy, neurodegenerative disease including amyotrophic  
 CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood  
 CC cells such as leukopenia including eosinopenia, basopenia,

CC Lymphopenia, monocytopenia, neutropenia, Alzheimer's disease,  
 CC Parkinson's disease, Huntington's disease and tumours. The sequences are  
 CC also useful for inducing angiogenesis for treating wounds, ulcers and  
 CC diabetic complications of sickle cell disease, for treating cardiac  
 CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases  
 CC involving cellular degeneration. Sequences AAU81220-AAU81284 represent  
 CC human and mouse anti-tcrK agonist monoclonal antibodies and antibody  
 CC fragments of the invention.  
 CC  
 XX Sequence 129 AA;  
 SQ  
 Query Match 81.0%; Score 493.5; DB 23; Length 129;  
 Best Local Similarity 77.0%; Pred. No. 4,4e-39;  
 Matches 94; Conservative 10; Mismatches 9; Indels 9; Gaps 2;  
 QY 2 ESGPGVLPACQTLSTSCAVSGGSIIRSGGYWMIHQHKGLEWIGYIYHSGNTYYPSTL 61  
 DB 7 ESGPGVLPKPSQTLSTCTVSGGSIIRSGGYWMIHQHKGLEWIGYIYHSGNTYYPSTL 66  
 QY 62 KSRIAMSVDTSENKFSRLNSVTADTAVYYCAR-----LDGY--TLDIWGOGTLVTV 112  
 DB 67 KSRVTISVDTSKNPSLKLSVTADTAVYYCARERIAAAGADYYNGLDVWGOGTLVTV 126  
 QY 113 SS 114  
 DB 127 SS 128  
 RESULT 15  
 ID AAB30584  
 AAB30584 standard; Protein; 126 AA.  
 AC AAB30584;  
 DT 19-MAR-2001 (first entry)  
 XX  
 DE A human variable heavy chain region of anti-IgB antibody.  
 XX  
 KM Anti-idiotypic antibody; C-epsilon3 region; immunoglobulin E; IgE;  
 KM anti-IgB antibody; mimobody; vaccine; allergy; asthma; atopic dermatitis;  
 KM rhinitis; chronic urticaria; food allergy; IgE-mediated disease;  
 KM passive immunisation.  
 KM  
 OS Homo sapiens.  
 XX  
 PN WO200063252-A1.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 12-APR-2000; 2000WO-EP03288.  
 XX  
 PR 14-APR-1999; 99GB-0008533.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Kricek F, Stadler B, Vogel M;  
 XX  
 DR WPI; 2000-687161/67.  
 DR N-PSDB; AAC62336.  
 XX  
 PT Novel anti-idiotypic antibody against antibodies which inhibit binding  
 PT of immunoglobulin E to its high affinity receptor, useful in vaccines  
 PT for treating diseases such as allergy, rhinitis, atopic dermatitis -  
 XX

PS Claim 4; Fig 5c; 73pp; English.

XX The present sequence represents a human variable heavy chain region of  
CC an anti-idiotypic antibody that interferes with the binding of the  
CC C-epsilon3 region of immunoglobulin (IgE) to the high affinity receptor  
CC for IgE, i.e. and anti-IgE antibody. Such an antibody is referred to  
CC as a mAbody. The anti-IgE antibody fragment is used as a vaccine, and  
CC as a pharmaceutical for treating IgE-mediated diseases such as allergy,  
CC in particular asthma, atopic dermatitis, rhinitis, chronic urticaria and  
CC food allergies. It is also used to treat IgE-mediated diseases. It is  
CC also used for raising polyclonal or monoclonal antibodies. The polyclonal  
CC or monoclonal antibodies obtained are useful for treating IgE-mediated  
CC diseases by passive immunisation.

XX Sequence 126 AA;

Query Match 80.5%; Score 490; DB 21; Length 126;

Best Local Similarity 75.4%; Pred. No. 9.2e-39;

Matches 92; Conservative 11; Mismatches 11; Indels 8; Gaps 1;

QY 1 LESGPGLYKPAQTLSLSCAVSGGSIKSGYTWIRHPGKLEWIGYIYHSGNTYNPS 60  
DB 5 LESGPGLYKPSPTLSLTCTVSGGSIKSGYTWIRHPGKLEWIGYIYHSGNTYNPS 64  
QY 61 LKSRVMSVDTSENKPSLRINSVTADPAVYCARLDG-----YTLDIWGQGLTVTV 112  
DB 65 LKSRVMSVDTSENKPSLRINSVTADPAVYCARLDG-----YTLDIWGQGLTVTV 124  
QY 113 SS 114  
DB 125 SS 126

Search completed: February 10, 2004, 18:36:08  
Job time : 63.3727 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:39:30 ; Search time 26.2545 Seconds  
(without alignments)  
909.160 Million cell updates/sec

Title: US-10-027-725A-7

Sequence: 1 LESGPGLVKPAQTSLSCAV.....RLDGTLDIWGQGLVTVSS 114 /

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 20938283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                | Description        |
|------------|-------|-------------|--------|-------------------|--------------------|
| 1          | 609   | 100.0       | 114    | US-10-027-725A-7  | Sequence 7, Appli  |
| 2          | 556   | 91.3        | 114    | US-10-027-725A-8  | Sequence 9, Appli  |
| 3          | 546   | 89.7        | 114    | US-10-027-725A-9  | Sequence 8, Appli  |
| 4          | 519   | 85.2        | 122    | US-10-309-762-147 | Sequence 147, App  |
| 5          | 518.5 | 85.1        | 121    | US-10-309-762-152 | Sequence 152, App  |
| 6          | 517.5 | 85.0        | 125    | US-10-309-762-11  | Sequence 11, Appli |
| 7          | 514.5 | 84.5        | 121    | US-10-309-762-151 | Sequence 151, App  |
| 8          | 512   | 84.1        | 118    | US-10-309-762-138 | Sequence 138, App  |
| 9          | 512   | 84.1        | 120    | US-10-309-762-13  | Sequence 13, Appli |
| 10         | 512   | 84.1        | 120    | US-10-309-762-144 | Sequence 144, App  |
| 11         | 509.5 | 83.7        | 123    | US-10-309-762-12  | Sequence 12, Appli |
| 12         | 508.5 | 83.5        | 123    | US-10-309-762-10  | Sequence 10, Appli |
| 13         | 508.5 | 83.5        | 123    | US-10-309-762-18  | Sequence 18, Appli |
| 14         | 508.5 | 83.5        | 123    | US-10-309-762-19  | Sequence 19, Appli |
| 15         | 508.5 | 83.5        | 125    | US-10-309-762-8   | Sequence 8, Appli  |

|    |       |      |     |                    |                    |
|----|-------|------|-----|--------------------|--------------------|
| 16 | 508.5 | 83.5 | 125 | US-10-309-762-16   | Sequence 16, Appli |
| 17 | 506.5 | 83.2 | 119 | US-10-309-762-131  | Sequence 131, App  |
| 18 | 506.5 | 83.0 | 119 | US-10-309-762-140  | Sequence 140, App  |
| 19 | 505   | 82.9 | 252 | US-09-880-748-1994 | Sequence 1994, App |
| 20 | 504.5 | 82.8 | 125 | US-10-309-762-153  | Sequence 153, App  |
| 21 | 504   | 82.8 | 120 | US-10-309-762-139  | Sequence 139, App  |
| 22 | 503.5 | 82.7 | 127 | US-10-309-762-14   | Sequence 14, Appli |
| 23 | 503   | 82.6 | 124 | US-10-309-762-75   | Sequence 75, Appli |
| 24 | 503   | 82.6 | 143 | US-10-309-762-96   | Sequence 96, Appli |
| 25 | 501.5 | 82.3 | 117 | US-10-330-613-13   | Sequence 13, Appli |
| 26 | 501.5 | 82.3 | 117 | US-10-330-613-13   | Sequence 13, Appli |
| 27 | 500.5 | 82.2 | 251 | US-10-120-414-75   | Sequence 75, Appli |
| 28 | 498.5 | 81.9 | 253 | US-09-880-748-1619 | Sequence 1619, App |
| 29 | 497   | 81.6 | 110 | US-10-309-762-7    | Sequence 74, Appli |
| 30 | 497   | 81.6 | 121 | US-10-308-817-137  | Sequence 137, App  |
| 31 | 496.5 | 81.5 | 123 | US-10-309-762-17   | Sequence 17, Appli |
| 32 | 496   | 81.4 | 123 | US-10-153-382-21   | Sequence 21, Appli |
| 33 | 495.5 | 81.4 | 123 | US-10-309-762-9    | Sequence 9, Appli  |
| 34 | 494.5 | 81.2 | 119 | US-10-330-613-25   | Sequence 25, Appli |
| 35 | 494.5 | 81.2 | 119 | US-10-330-530-25   | Sequence 25, Appli |
| 36 | 493   | 81.0 | 221 | US-09-972-656-80   | Sequence 80, Appli |
| 37 | 490   | 80.5 | 126 | US-09-974-449-6    | Sequence 6, Appli  |
| 38 | 489.5 | 80.4 | 117 | US-10-330-613-5    | Sequence 5, Appli  |
| 39 | 489.5 | 80.4 | 117 | US-10-330-530-5    | Sequence 5, Appli  |
| 40 | 489   | 80.3 | 118 | US-10-078-7578-52  | Sequence 52, Appli |
| 41 | 486   | 79.8 | 122 | US-10-309-762-15   | Sequence 15, Appli |
| 42 | 484   | 79.5 | 116 | US-10-309-762-127  | Sequence 127, App  |
| 43 | 482.5 | 79.2 | 118 | US-10-308-817-138  | Sequence 138, App  |
| 44 | 482   | 79.1 | 256 | US-09-880-748-1607 | Sequence 1607, App |
| 45 | 482   | 79.1 | 487 | US-09-800-729-145  | Sequence 145, App  |

## ALIGNMENTS

US-10-027-725A-7  
Sequence 7, Application US/10027725A  
Publication No. US20030082659A1  
GENERAL INFORMATION:  
APPLICANT: Flicker, Sabine  
TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof  
FILE REFERENCE: 25401-4  
CURRENT APPLICATION NUMBER: US/10/027,725A  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/259,436  
PRIOR FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-027-725A-7

Query Match 100.0%; Score 609; DB 15; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.8e-51;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGPGLVKPAQTSLSCAVSGSIRSGGYWMSWIRPGKLEWIGYIYHSGNTYVPS 60  
DB 1 LESGPGLVKPAQTSLSCAVSGSIRSGGYWMSWIRPGKLEWIGYIYHSGNTYVPS 60  
QY 61 LKSRIAMSVDTSENKFSRLNSVTAADTAAYVYCARLDGTYLDIWGQGLVTVSS 114  
DB 61 LKSRIAMSVDTSENKFSRLNSVTAADTAAYVYCARLDGTYLDIWGQGLVTVSS 114

RESULT 2  
US-10-027-725A-9  
Sequence 9, Application US/10027725A  
Publication No. US20030082659A1  
GENERAL INFORMATION:

```

; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific Igb-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-027-725A-9

```

|                       |              |           |            |            |
|-----------------------|--------------|-----------|------------|------------|
| Query Match           | 91.3%        | Score 556 | DB 15      | length 114 |
| Best Local Similarity | 90.4%        | Pred      | NO. 9e-46  |            |
| Matches 103           | Conservative | 5         | Mismatches | 6          |
|                       |              |           | Indels     | 0          |
|                       |              |           | Gaps       | 0          |

**Oy** 1 LESGPGLVMPDAQTSLSCAVSGGSTRGGGYWWSWRÖHPKGLKEIGIYHSGNTYNPS 60  
::: :  
**Db** 1 LESGPGLVMPDSITLCTVSGGSIRSGGYWWSWRÖPKGLEIGIYHSGNTYNPS 60

| Qy  | Db  |
|---|-----|
| 61 LKSIAMSDTSENKESLRNVTAAADTVVYCARLDGYLDIMWGQTLVTSS   | 114 |
| 114   |     |
| 61 LKSTVMSVDTSKNHFSLRLSSVTAADTVVYCARSDGYLDIMWGQTLVTSS | 114 |
| 114   |     |

```

RESULT 3
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: SeqId version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8

```

|                       |       |                    |        |                                 |
|-----------------------|-------|--------------------|--------|---------------------------------|
| Query Match           | 89.7% | Score 546;         | DB 15; | Length 114;                     |
| Best Local Similarity | 89.5% | Pred. No. 8.1e-45; |        |                                 |
| Matches               | 102;  | Conservative       | 4;     | Mismatches 8; Indels 0; Gaps 0; |

  

|    |    |   |     |
|----|----|---|-----|
| Qy | 1  | LESGGIVKPPQOTLSLCAVSGSGSRGSGYVSWMTIRHPGKLEKIGVYTHSGNRYNPS | 60  |
|    |    |   |     |
| Db | 1  | LESGGIVKPPQOTLSLCTVSGGSRGSGYVSWKPPGKLEKIGVYTHSGNRYNPS     | 60  |
|    |    |   |     |
| Qy | 61 | LKSRTIAMSVDTSSENKFSRLPLNSVTADPAVYYCAFLDGYTLDIWGGTLVTVSS   | 114 |
|    |    |   |     |
| Db | 61 | LKSRTIAMSVDTSSENKFSRLTSTVADPAVYYCASDGYTLDIWGGTLVTVSS      | 114 |
|    |    |   |     |

```

RESULT 4
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A

```

```

? CURRENT APPLICATION NUMBER: US/10/309,762
? CURRENT FILING DATE: 2002-12-02
? PRIOR APPLICATION NUMBER: 60/337275
? PRIOR FILING DATE: 2001-12-03
? NUMBER OF SEQ ID NOS: 246
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 147
? LENGTH: 122
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-309-762-147

```

|                       |                  |               |           |             |
|-----------------------|------------------|---------------|-----------|-------------|
| Query Match           | 85.2%            | Score 519;    | DB 12;    | Length 122; |
| Best Local Similarity | 81.2%            | Pred. No. 3   | 3e-47;    |             |
| Matches 95;           | Conservative 12; | Mismatches 6; | Indels 4; | Gaps 1;     |

QY 2 EESPGVLVPAQTLSTLSKAVSGGSIKRSAGYYWMIKROHPGKGLGEMIGYIYHSGNTYINPSSL 61  
Db 6 EESPGVLKPSQTLSTCTVSGGSISSGGYYWMIKROHPGKGLGEMIGYIYHSGSTYINPSSL 65

Qy 62 KSIPIAMSDTSEKFSRLNSTAADAIVYCAR----LDGTLDINGOGTLTVSS 114  
 66 KSRVTISDTSKQFSLKLSSTAAIDAIVYCARRYDILTGMDVMVGQITVSS 122  
 Db

```

RESULT 5
US-10-309-762-152
: Sequence 152: Application US/10309762
: Publication No. US20040018198A1
: GENERAL INFORMATION:
: APPLICANT: Gudas, Jean
: APPLICANT: Foltz, Ian
: APPLICANT: Handa, Masahisa
: APPLICANT: Gallo, Michael
: TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
: TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
: FILE REFERENCE: ARGENIX 027A
: CURRENT APPLICATION NUMBER: US/10/309,762
: CURRENT FILING DATE: 2002-12-02
: PRIOR APPLICATION NUMBER: 60/337275
: PRIOR FILING DATE: 2001-12-03
: NUMBER OF SEQ ID NOS: 246
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 152
: LENGTH: 121
: TYPE: PR1
: ORGANISM: Homo sapiens
US-10-309-762-152

```

|    |             |  |       |            |             |        |    |        |     |
|----|-------------|--|-------|------------|-------------|--------|----|--------|-----|
|    | Query Match | Similarity   | 85.1% | Score      | 518.5       | DB     | 12 | length | 121 |
|    | Best Local  | Similarity   | 81.9% | Pred.      | No. 3,76-42 |        |    |        |     |
|    | Matches     | Conservative   | % 11; | Mismatches | 7;          | Indels | 3; | Gaps   | 1;  |
| OY | 2           | ESGGGLVKKPQTTLSGCAVGGSGIRSGGYWWSWIROHFGKLEIGIYTHSGNYYNPSTL   | 61    |            |             |        |    |        |     |
| Db | 6           | ESGGGLVKKPQTTLSLTCTVSOGSSISCGGYWWSWIROHFGKLEIGIYTHSGNYYNPSTL | 65    |            |             |        |    |        |     |
| OY | 62          | KSRITAMSDVTSENKFSLRLNSVTAAADPAVYYCARLD--GTTLDDINOCGLTYVSS    | 114   |            |             |        |    |        |     |
| Db | 66          | KSRITATVDTSKNQPSLKLSSTVAADPAVYYCAYDILLTGAFIDIQGGTNAVYSS      | 121   |            |             |        |    |        |     |

```

: RESULT 6
: US-10-309-762-11
: Sequence 11, Application US/10309762
: Publication No. US20040018198A1
: GENERAL INFORMATION:
: APPLICANT: Gudas, Jean
: APPLICANT: Foltz, Ian
: APPLICANT: Handa, Masahisa
: APPLICANT: Gallo, Michael
: TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
: TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

```

FILE REFERENCE: AGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-11

Query Match 85.0%; Score 517.5; DB 12; Length 125;  
Best Local Similarity 81.7%; Pred. No. 4.7e-42;  
Matches 98; Conservative 9; Mismatches 6; Indels 7; Gaps 2;

Oy 2 ESGGGLVPAQTLISCAVSGSIRSGYWSWIRHPGKLEWIGYIYHSGNTYNNPSL 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 6 ESGGGLVPSQTLISCTVSGSISGGYWSWIRHPGKLEWIGYIYHSGNTYNNPSL 65  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Oy 62 KSRIAMSVDTSENKFSRLNSVTADTAIVYYCARL---LDGY--TLDIWGGTLVTYSS 114  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 66 KSRIATISVDTSKNQFSLKLSVTADTAIVYYCARTYDFLIGYDPADPWGQGLVTYSS 125  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7  
US-10-309-762-151  
Sequence 151, Application US/10309762  
Publication No. US20040018198A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: AGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 151  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-151

Query Match 84.5%; Score 514.5; DB 12; Length 121;  
Best Local Similarity 81.0%; Pred. No. 8.9e-42;  
Matches 94; Conservative 13; Mismatches 6; Indels 3; Gaps 1;

Oy 2 ESGGGLVPAQTLISCAVSGSIRSGYWSWIRHPGKLEWIGYIYHSGNTYNNPSL 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 6 ESGGGLVPSQTLISCTVSGSISGGYWSWIRHPGKLEWIGYIYHSGNTYNNPSL 65  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Oy 62 KSRIAMSVDTSENKFSRLNSVTADTAIVYYCARL---DGYTLDIWGGTLVTYSS 114  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 66 KSRIATISVDTSKNQFSLKLSVTADTAIVYYCARVLLMFGMDWGGQGLVTYSS 121  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8  
US-10-309-762-138  
Sequence 138, Application US/10309762  
Publication No. US20040018198A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN  
FILE REFERENCE: AGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 138  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-138

Query Match 84.1%; Score 512; DB 12; Length 118;  
Best Local Similarity 83.2%; Pred. No. 1.5e-41;  
Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Oy 2 ESGGGLVPAQTLISCAVSGSIRSGYWSWIRHPGKLEWIGYIYHSGNTYNNPSL 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 6 ESGGGLVPSQTLISCTVSGSISGGYWSWIRHPGKLEWIGYIYHSGNTYNNPSL 65  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Oy 62 KSRIAMSVDTSENKFSRLNSVTADTAIVYYCARL---LDGY--TLDIWGGTLVTYSS 114  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 66 KSRIATISVDTSKNQFSLKLSVTADTAIVYYCARTYDFLIGYDPADPWGQGLVTYSS 118  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9  
US-10-309-762-13  
Sequence 13, Application US/10309762  
Publication No. US20040018198A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: AGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-13

Query Match 84.1%; Score 512; DB 12; Length 120;  
Best Local Similarity 81.9%; Pred. No. 1.5e-41;  
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

Oy 2 ESGGGLVPAQTLISCAVSGSIRSGYWSWIRHPGKLEWIGYIYHSGNTYNNPSL 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 6 ESGGGLVPSQTLISCTVSGSISGGYWSWIRHPGKLEWIGYIYHSGNTYNNPSL 65  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Oy 62 KSRIAMSVDTSENKFSRLNSVTADTAIVYYCARL---LDGY--TLDIWGGTLVTYSS 114  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 66 KSRIATISVDTSKNQFSLKLSVTADTAIVYYCARL---DGYTLDIWGGTLVTYSS 120  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10  
US-10-309-762-144  
Sequence 144, Application US/10309762  
Publication No. US20040018198A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael





APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 19  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-19

Query Match 83.5%; Score 508.5; DB 12; Length 123;  
Best Local Similarity 80.5%; Pred. No. 3.4e-41;  
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

QY 2 ESGPGLVPRPAQTLSICAVSGSIRSGYWSMIRQHPGKLEWIGIYHSGNTYYNPBL 61  
DB 6 ESGPGLVPRSQTLSTCTVSGSINGGYWSMIRQHPGKLEWIGIYHSGSTYYNPBL 65  
QY 62 KSRIMSVDTSENKPSLRINSTYADTAVYYCAR-----LDGYTLIDWGQGLTVVSS 114  
DB 66 KSRVITISVDTSENQPSLKLSTYADTAVYYCARRRVTDYVYGLDVGQGLTVVSS 123

## RESULT 15

US-10-309-762-8  
Sequence 8, Application US/10309762  
Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Folz, Jean  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-8

Query Match 83.5%; Score 508.5; DB 12; Length 125;  
Best Local Similarity 79.2%; Pred. No. 3.4e-41;  
Matches 95; Conservative 12; Mismatches 6; Indels 7; Gaps 2;

QY 2 ESGPGLVPRPAQTLSICAVSGSIRSGYWSMIRQHPGKLEWIGIYHSGNTYYNPBL 61  
DB 6 ESGPGLVPRSQTLSTCTVSGSINGGYWSMIRQHPGKLEWIGIYHSGSTYYNPBL 65  
QY 62 KSRIMSVDTSENKPSLRINSTYADTAVYYCAR-----LDGYTLIDWGQGLTVVSS 114  
DB 66 KSRVITISVDTSENQPSLKLSTYADTAVYYCARFYDILGYPDAFDIWGQGLTVVSS 125

Search completed: February 10, 2004, 19:03:02  
Job time : 33.2545 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 ; Search time 11.7455 Seconds  
(without alignments)  
410.664 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609  
Sequence: 1 LESGPGLVKPAQTSLSCAV.....RLDGTLDIMGQGLVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfill1es1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Query length | DB ID | Description        |
|------------|-------|-------------|--------------|-------|--------------------|
| 1          | 499   | 81.9        | 473          | 3     | US-09-049-672A-4   |
| 2          | 471.5 | 77.4        | 119          | 1     | US-08-360-125-5    |
| 3          | 471.5 | 77.4        | 119          | 2     | US-08-450-578-5    |
| 4          | 471.5 | 77.4        | 119          | 2     | US-09-017-628-5    |
| 5          | 471.5 | 77.4        | 119          | 2     | US-09-014-880-5    |
| 6          | 471.5 | 77.4        | 119          | 4     | US-09-025-769B-39  |
| 7          | 471.5 | 77.4        | 119          | 4     | US-09-025-769B-65  |
| 8          | 471.5 | 77.4        | 119          | 4     | US-08-450-363-5    |
| 9          | 466   | 76.5        | 122          | 1     | US-08-360-125-11   |
| 10         | 466   | 76.5        | 122          | 2     | US-08-450-578-11   |
| 11         | 466   | 76.5        | 122          | 2     | US-09-017-628-11   |
| 12         | 466   | 76.5        | 122          | 2     | US-09-014-880-11   |
| 13         | 466   | 76.5        | 122          | 4     | US-08-450-363-11   |
| 14         | 455   | 74.7        | 118          | 4     | US-09-025-769B-25  |
| 15         | 453   | 74.4        | 118          | 4     | US-08-545-809A-116 |
| 16         | 446.5 | 73.3        | 250          | 4     | US-10-039-785-50   |
| 17         | 445   | 73.1        | 244          | 4     | US-08-918-148-79   |
| 18         | 442.5 | 72.7        | 142          | 2     | US-08-480-774A-2   |
| 19         | 438   | 71.9        | 278          | 3     | US-09-260-527-3    |
| 20         | 429.5 | 70.5        | 119          | 2     | US-08-652-816A-10  |
| 21         | 429   | 70.4        | 150          | 4     | US-09-582-337-14   |
| 22         | 427   | 70.1        | 118          | 4     | US-09-343-698-6    |
| 23         | 425.5 | 69.9        | 476          | 4     | US-08-487-550-12   |
| 24         | 425.5 | 69.6        | 476          | 4     | US-09-526-098-12   |
| 25         | 424   | 69.6        | 118          | 3     | US-08-545-809A-142 |
| 26         | 422.5 | 69.4        | 98           | 1     | US-08-478-039-75   |
| 27         | 422.5 | 69.4        | 98           | 1     | US-08-476-349A-75  |

|    |       |      |     |   |                    |                   |
|----|-------|------|-----|---|--------------------|-------------------|
| 28 | 422   | 69.3 | 126 | 1 | US-08-276-852-142  | Sequence 142, App |
| 29 | 422   | 69.3 | 126 | 1 | US-08-899-575-142  | Sequence 142, App |
| 30 | 422   | 69.3 | 126 | 5 | US-08-899-575-142  | Sequence 142, App |
| 31 | 422   | 69.3 | 126 | 5 | PCT-US95-08743-142 | Sequence 142, App |
| 32 | 420.5 | 69.0 | 124 | 1 | US-08-478-039-78   | Sequence 78, Appl |
| 33 | 420.5 | 69.0 | 124 | 1 | US-08-476-349A-78  | Sequence 78, Appl |
| 34 | 420   | 69.0 | 832 | 3 | US-08-630-820-7    | Sequence 37, Appl |
| 35 | 419.5 | 68.9 | 219 | 4 | US-09-460-384-37   | Sequence 27, Appl |
| 36 | 418.5 | 68.7 | 96  | 3 | US-08-851-362D-27  | Sequence 44, Appl |
| 37 | 418.5 | 68.7 | 117 | 3 | US-08-851-362D-44  | Sequence 44, Appl |
| 38 | 418.5 | 68.7 | 123 | 4 | US-08-793-450-4    | Sequence 4, Appl  |
| 39 | 418.5 | 68.7 | 472 | 4 | US-08-793-450-8    | Sequence 4, Appl  |
| 40 | 418   | 68.6 | 244 | 4 | US-10-039-785-44   | Sequence 44, Appl |
| 41 | 415   | 68.1 | 118 | 3 | US-08-545-809A-123 | Sequence 123, App |
| 42 | 414   | 68.0 | 119 | 1 | US-08-478-039-77   | Sequence 77, Appl |
| 43 | 414   | 68.0 | 119 | 1 | US-08-476-349A-77  | Sequence 77, Appl |
| 44 | 410.5 | 67.4 | 467 | 3 | US-08-523-894-8    | Sequence 8, Appl  |
| 45 | 410.5 | 67.4 | 467 | 3 | US-08-523-894-10   | Sequence 10, Appl |

## ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
Sequence 4, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Yang, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049, 672A  
FILING DATE: HEREMITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PR-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANCYTUT01

CLONE: 1513264  
US-09-049-672A-4  
Query Match 81.9%; Score 499; DB 3; Length 473;  
Best Local Similarity 78.2%; Pred. No. 2.7e-43;  
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;  
QY 2 ESGPGLVKPAQTLISCAVSGSIRSGYYWMIROHPGKLEWIGYIYHSGNTYYPNL 61  
DB 25 ESGPGLVKPSESLTICAVSGSITSGGYWMIROHPGKLEWIGYIYHSGNTYYPNL 84  
62 KSRIMSVDTSENKFSRLNSVTADTAVYVCARDL-----GYTLDMGQGLTVTVSS 114  
QY 85 KSRVTSISVTSKQFSLKLSVTADTAVYVCARDVGLRGNGYGMVWGQGLTVTVSS 143  
DB  
RESULT 2  
US-08-360-125-5  
Sequence 5, Application US/08360125  
Patent No. 5767246  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246hiko ITO  
APPLICANT: Kazuhiko NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:  
HABITTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLER:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-5  
Query Match 77.4%; Score 471.5; DB 1; Length 119;  
Best Local Similarity 75.9%; Pred. No. 3.5e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;  
QY 2 ESGPGLVKPAQTLISCAVSGSIRSGYYWMIROHPGKLEWIGYIYHSGNTYYPNL 61  
DB 6 ESGPGLVKPQTLISCTVSGSISCGFYWMIRHPGKLEWIGYIYHSGNTYYPNL 65  
QY 62 KSRIMSVDTSENKFSRLNSVTADTAVYCA---RLDGYTLDMGQGLTVTVSS 114  
DB 66 KSRVTSISVTSKQFSLKLSVTADTAVYCARSTRLNG--ADYWGQGLTVTVSS 119  
RESULT 3  
US-08-450-578-5  
Sequence 5, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845hiko ITO  
APPLICANT: Kazuhiko NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:

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1 APPLICATION NUMBER: US/08/450,578
2 FILING DATE: May 25, 1995
3 CLASSIFICATION: 435
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: 08/360,125
6 FILING DATE: December 20, 1994
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 07/995,534
9 FILING DATE: June 29, 1992
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Warren M. Cheek, Jr.
12 REGISTRATION NUMBER: 33,367
13 REFERENCE/DOCKET NUMBER:
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 202-371-8850
16 TELEFAX:
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18 INFORMATION FOR SEQ ID NO: 5:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 119 amino acids
21 TYPE: amino acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: protein
25 HYPOTHEetical:
26 ANTI-SENSE:
27 FRAGMENT TYPE:
28 ORIGINAL SOURCE:
29 ORGANISM:
30 STRAIN:
31 INDIVIDUAL ISOLATE:
32 DEVELOPMENTAL STAGE:
33 HAPLOTYPE:
34 TISSUE TYPE:
35 CELL TYPE: Hybridoma producing human
36 CELL TYPE: antibody GAH
37 CELL LINE:
38 ORGANELLE:
39 IMMEDIATE SOURCE:
40 LIBRARY:
41 CLONE:
42 POSITION IN GENOME:
43 CHROMOSOME/SEGMENT:
44 MAP POSITION:
45 UNITS:
46 FEATURE:
47 NAME/KEY:
48 LOCATION:
49 IDENTIFICATION METHOD:
50 OTHER INFORMATION:
51 PUBLICATION INFORMATION:
52 AUTHORS:
53 TITLE:
54 JOURNAL:
55 VOLUME:
56 ISSUE:
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|                       |       |   |      |                  |
|-----------------------|-------|---|------|------------------|
| Query Match           | 77.4% | Score 471.5   | DB 2 | Length 119       |
| Best Local Similarity | 75.9% | Pred. No. 3.5e-41   |      |                  |
| Matches               | 88    | Conservative  | 7    | Indels 5; Gaps 2 |
| Qy                    | 2     | ESGGLVLPACTTSLSCAVSGSINSGGYTWIMIHQHKGLKLEWIGYTHSGNTYYNBSL | 61   |                  |
|                       |       |   |      |                  |
| Db                    | 6     | ESGFLVLPVSQTLSTCTVSGSGISCCGFMWIMIQHKGLKLEWIGYTHYSSTYYNBSL | 65   |                  |
|                       |       |   |      |                  |
| Oy                    | 62    | KSRIAMSVDSSENKFLRLNSVTAADTVAYYCA--RLDGYTLIDIGQGLTVASS     | 114  |                  |

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Db      66 KSRVTISLDTSKQFSLKLSLPTADTA VVYCARSTRLRG--ADYWGQGTMTVTS 119

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RESULT 4
US-09-017-628-5
Sequence 5, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287@hiko
APPLICANT: NAGAIKE, Kazuhiko
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 119
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5

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```

Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 75.9%; Pred. No. 3.5e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2

Oy      2  ESEPGLYKPMQTSLSCAVSGGSTRSGCYWSMIRHPGKLEIMIGYIHSGNTYTNPSL 61
Db      6  EESGGVLKPPQITSLTCTVSGGSISSCGFYNNWIRHKGKLEIMIGYIYSGSTYTNPSL 65
Oy      62 KSRIAMVSDISENFSLRINSVTADAVVYCA--RLDGYTLIDWGGTLVTVSS 114
Db      66 KSRVITSLDPSKQFSLKLSLTADIAVYCASTRLRG--ADYWGQTVTVYSS 119

RESULT 5
US-09-014-880-5
; Sequence 5, Application US/09014880
; Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Marlen M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
US-09-014-880-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;  
Best Local Similarity 75.9%; Pred. No. 3.5e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGVLPKPAQLTSLSCAVSGSIRSGGYWMIHQPGKLEWIGIYHSNTYNNPSL 61  
DB 6 ESGPGVLPKSPQTLSTLCVSGSISGCFYWNIRHPGKLEWIGIYHSNTYNNPSL 65  
QY 62 KSRIMSVDTSENKFSRLNSVTADTAIVYCA---RLDGIYDGGGLTVTSS 114  
DB 66 KSRVITSLDTSKQPSFKLSLTAADTAIVYCAARSTRLENG--ADYWGQGTMTVSS 119

RESULT 6  
US-09-025-769B-39  
Sequence 39, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilaq, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 77.4%; Score 471.5; DB 4; Length 119;  
Best Local Similarity 77.6%; Pred. No. 3.5e-41;  
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

QY 2 ESGPGVLPKPAQLTSLSCAVSGSIRSGGYWMIHQPGKLEWIGIYHSNTYNNPSL 61  
DB 6 ESGPGVLPKSPQTLSTLCVSGSISGCFYWNIRHPGKLEWIGIYHSNTYNNPSL 63  
QY 62 KSRIMSVDTSENKFSRLNSVTADTAIVYCARLDG---YTLDIWGGGLTVTSS 114  
DB 64 KSRVITSLDTSKQPSFKLSLTAADTAIVYCAARWGSGFYAMDYWGQGLTVTSS 119

RESULT 7  
US-09-025-769B-65  
Sequence 65, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilaq, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-65

Query Match 77.4%; Score 471.5; DB 4; Length 119;  
Best Local Similarity 77.6%; Pred. No. 3.5e-41;

CELL TYPE: Hybridoma producing human

PRIOR APPLICATION DATA:





OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-11

Query Match  
Best Local Similarity 76.5%; Score 466; DB 2; Length 122;  
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMIROHPKGLGEMIGYIHSNTYYPNSL 61  
DB 6 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMIROHPKGLGEMIGYIHSNTYYPNSL 65

QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCAR--LDG--YTLDDIWGGTLVTVSS 114  
DB 66 KSRVTISVDTSKNQFSKLKLSVTADTAAYVYCARSGYGGYGMVWGQGTTVTVSS 122

RESULT 11  
US-09-017-628-11  
Sequence 11, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287jnhiko  
APPLICANT: NAGAIKE, Kazuhiko  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
FILE REFERENCE: 177/527361KH  
CURRENT FILING DATE: 1998-02-02  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1  
US-09-017-628-11

Query Match  
Best Local Similarity 76.5%; Score 466; DB 2; Length 122;  
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMIROHPKGLGEMIGYIHSNTYYPNSL 61  
DB 6 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMIROHPKGLGEMIGYIHSNTYYPNSL 65

QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCAR--LDG--YTLDDIWGGTLVTVSS 114  
DB 66 KSRVTISVDTSKNQFSKLKLSVTADTAAYVYCARSGYGGYGMVWGQGTTVTVSS 122

RESULT 12  
US-09-014-880-11  
Sequence 11, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 203 R Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
US-09-014-880-11

Query Match  
Best Local Similarity 76.5%; Score 466; DB 2; Length 122;  
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMIROHPKGLGEMIGYIHSNTYYPNSL 61  
DB 6 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMIROHPKGLGEMIGYIHSNTYYPNSL 65

QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCAR--LDG--YTLDDIWGGTLVTVSS 114  
DB 66 KSRVTISVDTSKNQFSKLKLSVTADTAAYVYCARSGYGGYGMVWGQGTTVTVSS 122

RESULT 13  
US-08-450-363-11  
Sequence 11, Application US/08450363  
Patent No. 6436434  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 6436434ihiko ITO  
APPLICANT: Kazuhiko NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Cell Membrane  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack  
 STREET: 805 Fifteenth Street, N.W., #700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/450,363  
 FILING DATE: May 25, 1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/360,125  
 FILING DATE: December 20, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/905,534  
 FILING DATE: June 29, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-8850  
 TELEFAX:  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 122 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL:  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE: Hybridoma producing human antibody 1-3-1-1  
 CELL LINE:  
 ORGANELLAE:  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 CLONE:  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT:  
 MAP POSITION:  
 UNITS:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:

;  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-11

|                       |                  |                    |           |             |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match           | 76.5%;           | Score 466;         | DB 4;     | Length 122; |
| Best Local Similarity | 75.2%;           | Pred. No. 1.3e-40; |           |             |
| Matches 88;           | Conservative 13; | Mismatches 12;     | Indels 4; | Gaps 2.     |

Qy 2 ESGPGLVKPAOTLSLSCAVSGSIRSGGYWMSNRQHPKGLGWYGYIYHSNGTYNPSL 61

Db 6 ESGPGLVKPSTLSLCTVSGSISSSSYWGWIRQPPKGLGWIGSIYVSGSTYNP 65

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QY      62 KSRILAMSVDTSENKFSRLRLNSVTAADTAVYYCAR--LDG--YTLIDIWGGGLTVRVSS 114
      |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66 KSRVTIISVDTISKNGFSLKLSSVTAADTAVYYCARGSYGGYYGMDWGGGTTTVVSS 122

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RESULT 14  
US-09-025-769B-25

```

; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
;

```

Ge, Liming  
Moroney, Simon  
APPLICANT: ;  
APPLICANT: ;

[illegible]

CITY: New York  
STATE: New York

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; CONVERTING FROM ASCII TO

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```

;
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 115/06/035 769B

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18 AUG 1995

NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794

TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEC ID NO: 35.

```

; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS:

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MOLECULE TYPE: protein  
US-09-025-769B-25

Best Local Similarity: 77.4%; Pred. No. 1.7e-39;  
Matches 89; Conservative 10; Mismatches 12; Indels 4; Gaps 2

Db

6 ESGPGIVKPSSEILSLICTVSGGSISS--YMSWIRQPPGKGLWGIYHSGSTNNYPSL 6

Oy 62 KSRIAMVDTSSEKSLINSVTAADPAVYYCA--RLDGYTLIDIMGOSTLVTVSS 114  
 Db 64 KSRVTISVDTSKNGPSLKLSSVTADPAVYYCARGGGGVFDYMGOSTLVTVSS 118

RESULT 15

US-08-545-809A-116  
 ; Sequence 116 Application US/08545809A  
 ; Patent No. 6096878  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Honjo, Yasuko  
 ; APPLICANT: Matsuda, Fumihiko  
 ; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
 ; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
 ; NUMBER OF SEQUENCES: 145  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson, P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: US  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/545, 809A  
 ; FILING DATE: 27-MAR-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/JP93/00603  
 ; FILING DATE: 10-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Freeman, John W.  
 ; REGISTRATION NUMBER: 29, 066  
 ; REFERENCE/DOCKET NUMBER: 06501/004001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-542-5070  
 ; TELEFAX: 617-542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 116:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 118 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-545-809A-116

Query Match 74.4%; Score 453; DB 3; Length 118;  
 Best Local Similarity 86.2%; Pred. No. 2.7e-39;  
 Matches 81; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ESGGLVPAQTLISCAVSGSIRSGYVSWIRQHPKGLWIGYIYHSGNTYVNPSTL 61  
 Db 25 ESGGLVPSQTLISCTVSGSISGGSYVSWIRQHPKGLWIGYIYHSGNTYVNPSTL 84  
 Oy 62 KSRIAMVDTSSEKSLINSVTAADPAVYYCA 95  
 Db 85 KSRVTISVDTSKNGPSLKLSSVTADPAVYYCAR 118

Search completed: February 10, 2004, 18:42:06  
 Job time : 19.7455 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 11.7455 Seconds  
(without alignments)  
933.402 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614  
Sequence: 1 EESGRLVPSQTSLTCTV.....RSDGTYLDNMGGTLVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID  | Description        |
|------------|-------|---------|--------------|--------|--------------------|
| 1          | 499.5 | 81.4    | 135          | S78051 | Ig heavy chain pre |
| 2          | 495.5 | 80.7    | 147          | S13519 | Ig heavy chain V r |
| 3          | 487   | 79.3    | 130          | S30534 | Ig heavy chain V r |
| 4          | 480.5 | 78.3    | 121          | S44113 | Ig heavy chain V r |
| 5          | 478.5 | 77.9    | 140          | I37782 | Ig variable region |
| 6          | 477.5 | 77.8    | 146          | S09710 | Ig heavy chain V r |
| 7          | 474.5 | 77.3    | 116          | S37456 | Ig mu chain - huma |
| 8          | 474.5 | 77.3    | 130          | S31690 | Ig heavy chain V r |
| 9          | 474   | 77.2    | 122          | S69912 | Ig V-D-J region (N |
| 10         | 473.5 | 77.1    | 128          | S31514 | Ig heavy chain - h |
| 11         | 472.5 | 77.0    | 127          | S19668 | Ig heavy chain V r |
| 12         | 469   | 76.4    | 137          | S31676 | Ig heavy chain V r |
| 13         | 468.5 | 76.3    | 123          | S30530 | Ig heavy chain V r |
| 14         | 465.5 | 75.8    | 155          | S31511 | Ig heavy chain - h |
| 15         | 463.5 | 75.5    | 155          | S31512 | Ig heavy chain - h |
| 16         | 462   | 75.2    | 139          | S31586 | Ig heavy chain V r |
| 17         | 460.5 | 75.0    | 146          | S09711 | Ig heavy chain V r |
| 18         | 460   | 74.9    | 145          | S78055 | Ig heavy chain pre |
| 19         | 459.5 | 74.8    | 109          | PH1673 | Ig heavy chain V r |
| 20         | 457   | 74.4    | 110          | S44110 | Ig heavy chain V-D |
| 21         | 455   | 74.1    | 99           | S26803 | Ig heavy chain V r |
| 22         | 454   | 73.9    | 139          | A41287 | Ig heavy chain pre |
| 23         | 453   | 73.8    | 99           | S26801 | Ig heavy chain V r |
| 24         | 452   | 73.6    | 129          | S44114 | Ig heavy chain V r |
| 25         | 450   | 73.3    | 99           | S26802 | Ig heavy chain V r |
| 26         | 450   | 73.3    | 135          | S31604 | Ig heavy chain V r |
| 27         | 447   | 72.8    | 118          | S20780 | Ig heavy chain V r |
| 28         | 446   | 72.6    | 99           | S12418 | Ig heavy chain V r |
| 29         | 444.5 | 72.4    | 139          | S31696 | Ig heavy chain V r |

|    |       |      |     |   |        |                    |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 443   | 72.1 | 118 | 2 | A26340 | Ig heavy chain pre |
| 31 | 442.5 | 72.1 | 140 | 2 | A49045 | Ig heavy chain V r |
| 32 | 441.5 | 71.9 | 132 | 2 | A38911 | Ig heavy chain V r |
| 33 | 441   | 71.8 | 99  | 2 | S26800 | Ig heavy chain V r |
| 34 | 441   | 71.8 | 126 | 2 | S47010 | Ig heavy chain V4. |
| 35 | 440.5 | 71.7 | 129 | 1 | D2HWA  | Ig heavy chain V-I |
| 36 | 440   | 71.7 | 97  | 2 | PL0118 | Ig heavy chain V-I |
| 37 | 440   | 71.7 | 99  | 2 | S26899 | Ig heavy chain V r |
| 38 | 439.5 | 71.6 | 98  | 2 | S12421 | Ig heavy chain V r |
| 39 | 439.5 | 71.6 | 140 | 2 | A4770  | hypothetical hybr  |
| 40 | 439   | 71.5 | 140 | 2 | S78052 | Ig heavy chain pre |
| 41 | 438.5 | 71.4 | 123 | 2 | S30529 | Ig heavy chain V r |
| 42 | 438   | 71.3 | 120 | 2 | PR0370 | Ig mu chain precu  |
| 43 | 437   | 71.2 | 124 | 2 | S31684 | Ig heavy chain V r |
| 44 | 435.5 | 70.9 | 134 | 2 | S54906 | Ig heavy chain V r |
| 45 | 434.5 | 70.8 | 98  | 2 | S26902 | Ig heavy chain V r |

## ALIGNMENTS

```
RESULT 1
Ig heavy chain precursor V-D-J region (clone mab 61VH) - human (Fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78051; S23716
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78051
A:Molecule type: mRNA
A:Residues: 1-135 <HAR>
A:Cross-references: EMBL:X54437, NID:G37814, PID:CA48306.1, PID:G930117
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A>Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23716
A:Molecule type: mRNA
A:Residues: 13-111 <HAW>
A:Cross-references: EMBL:X54437
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:27-111/Domain: immunoglobulin homology <IMM>

Query Match      81.4%  Score 499.5; DB 2; Length 135;
Best Local Similarity 79.7%  Pred. No. 9.3e-38;
Matches 94; Conservative 10; Mismatches 9; Indels 5; Gaps 2;

QY 2 EESGRLVPSQTSLTCTVSGSIRSGYSWYROPKGKLEWIGNIYHSGNTYPSL 61
DB 18 EESGRLVPSQTSLTCTVSGSIRSGYHWYROPKGKLEWIGNIYHSGNTYPSL 77
QY 62 KSRITMSVDTSKNHFSLRLSVTAADPAVYCAR--SDGYTLDN---WGOGTLVTVSS 114
DB 78 KSRITMSVDTSKNHFSLRLSVTAADPAVYCARLGPDPDYTLDMVDVWGOGTLVTVSS 135

RESULT 2
S13519
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S13519
R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A>Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A:Reference number: S13519; MUID:91187691; PMID:2011536
A:Accession: S13519
```

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-147 <EMBL>  
A:Cross-references: EMBL:X65158, NID:g37724, PTD:CAA39626.1, PID:g37725  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:41-125/Domain: immunoglobulin homology <IIM>

|                       |        |                    |       |                  |
|-----------------------|--------|--------------------|-------|------------------|
| Query Match           | 80.7%  | Score 495.5;       | DB 2; | Length 147;      |
| Best Local Similarity | 80.2%; | Pred. No. 2.3e-37; |       |                  |
| Matches               | 93;    | Mismatches         | 11;   | Indels 3; Gaps 1 |

```

Oy      2  ESGPGLVKPSQRLSLTCTVSGGSLRSGGYWMSWRQPPGKGLWIGNIYHSGNTYNNPSL 61
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      32  ESGPGLVKPSETLSLTCTVSGGSLSSSSYYWGWIRQPPGKGLWIGSIYYSGSTYNNPSL 91

```

```
Oy      62 KSRITMVDTSKNHPSLRITSVTADTA VVYCAR---DGYTLDNMGOGT LVTVSS   114
        ||::|||||    ||::|||||    |   |||||
Db      92 KSRVTISVDTSKQFSLKLTSSVTADTA VVYCARPLIMFGELFDYWGOGT LVTVSS   147
```

RESULT 3  
S30534  
Ig heavy chain V region - human  
C1Species: Homo sapiens (man)  
C1Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
CAccession: S30534  
R1Mariette, X.

submitted to the EMBL Data Library, October 1992  
A/Reference number: S30520  
A/Accession: S30534  
A/Status: preliminary

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-110 <MAR>  
A:Cross-references: EMBL:Z18320  
C:Superfamily: immunoglobulin V region; immunoglobulin  
C:Keywords: heterotetramer; immunoglobulin  
P:15-99/Domain: immunoglobulin homology <IMM>

|                       |                 |                    |            |             |
|-----------------------|-----------------|--------------------|------------|-------------|
| Query Match           | 79.3%           | Score 487;         | DB 2;      | Length 130; |
| Best Local Similarity | 76.0%           | Pred. No. 1.2e-36; |            |             |
| Matches 95;           | Conservative 7; | Mismatches 11;     | Indels 12; | Gaps 2;     |

Qy 2 ESGPGLVKKPSTLTSLTCTVSGSIRSGGYWVVRQRPKGLGEMIGNIYHSGNTYVNSL 61

Ddb 6 ESGPGLVKKPSTLTSLTCTVSGSIRSSSYWVWIRQPAKGKLEIGRIYTTSGSINYNPSL 65

```

Qy      62  KSRIMSVDPNSKHNHFLRLSTVAATTAATVAVVYCARSG-----YT-----LDNMGGTL 109
Db      66  KSRIVISVDTSKNQFSLKLSTTAATTAATVAVVYCARDKGGFWGSGYTRNSRAAFIDWGGTM 125

```

|    |     |      |     |
|----|-----|------|-----|
| QY | 110 | VTSS | 114 |
|    |     |      |     |
| Db | 126 | VTSS | 130 |

RESULT 4  
S44113  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C>Date: 13-Jan-1995 #sequence \_revision 13-Jan-1995 #text\_change 24-May-2001  
C:Accession: S44113  
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r  
A:Reference number: S44105

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-121 <HAM>  
A:Cross-references: EMBL:Z31389; NID:G472967; PIDD:CA83264.1; PID:G940524  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:keywords: heterotetramer; immunoglobulin

F;15-99/Domain: immunoglobulin homology <IMM>

|                          |       |                    |           |             |
|--------------------------|-------|--------------------|-----------|-------------|
| Query Match              | 78.3% | Score 480.5;       | DB 2;     | Length 121; |
| Best Local Similarity    | 78.4% | Pred. No. 4.1e-36; |           |             |
| Matches 91; Conservative | 9;    | Mismatches 13;     | Indels 3; | Gaps 2;     |

**Qy**

2 ESGPGIVKPSOTLSLTCTVSGSIRSGGYWMSWRQPPEKGLEWIGNIYHSGNTYYNPSL 61  
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

**Dd**

6 ESGPGLVKPSTLSLTCTVSGGISSSYIWGMTRQPPGKGLEWIGSIYYSGSTYYNPSSL 65

```

Oy      62 KSRITMSVDTSKDNHFSRLTSTVTAADTAVYYCAR-SDGY--TLDNMGCGTLVTWSS 114
        |||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Db      66 KSRVITLSDTSKNQVSLKLTSSVTAADTGYRCSRLSGGYSDFDYMQGTLVTWSS 122

```

RESULT 5  
I37782

IG variable region (VDJ) (clone T23-9) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C/Accession: J37782, J52476  
R/Denatson, C.; Chastagner, P.; There, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A/Title: Somatic diversification in the heavy chain variable region genes of  
Reference number: A36876; MIMD:J94119917; PMID:8290556

A:Accession: I37782  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-References: EMBL:X67906; NID:g33582; PIDD:CAA4104.1; PID:g33583  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:46-128/Domain: Immunoglobulin homology <IM>

|                       |                 |                    |           |             |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match           | 77.9%;          | Score 478.5;       | DB 2;     | Length 140; |
| Best Local Similarity | 78.8%;          | Pred. No. 7.2e-36; |           |             |
| Matches 93;           | Conservative 9; | Mismatches 9;      | Indels 7; | Gaps 2      |

**Qy**      2    ESGPGLVKPSQTLSLTCTVSGGSIRGGYYWSWAPPPKGLEWIGNIYHSGNTYYNPSL 6  
               : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
**Dd**      25   ESGPGLVKPSLETSLTCTVSGGSSIS--YWMSWIROPKGLGEWIGIYYSGSNTNYNPSL 8

```

QY      62  KSRITNSVDTSKNHFSRLRLTSVTAADTA VYVCARSD ---GYTLDNNGOGLTVVSS 114
      |||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Db      83  KSRVITSVDTSKNQFSLKLSVTAADTA VYVCARHNSSSWGRYPDYNGOGLTVTVSS 140

```

```

RESULT 6
S09710      Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S09710
C: Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

```

A:Title: Nucleotide sequences and three-dimensional mod  
A:Reference number: S09710; MUID:90262535; PMID:2111699  
A:Accession: S09710

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1146 <IMG>  
C:Cross-References: GB:X52110; NID:g31447; PID:CA36344.1; PID:g31448  
A:Crossfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
A:34-118/Domain: immunoglobulin homology <IMG>

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 77.8%            | Score 477.5;       | DB 2;      | Length 146; |
| Best Local Similarity | 73.2%            | Pred. No. 9.3e-36; |            |             |
| Matches 90;           | Conservative 13; | Mismatches 9;      | Indels 11; | Gaps 2      |

QY 2 ESGPGLVKPSQTLSLTCTVSGSIRSCGYWMSWRQPCKGKLEWIGNIYHSGNTYYNPSL 61  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 25 ESGPGLVKPSTLSLTCTSVSGSGSGLYMGWTRQPPCKGLEWIGSI FYSGSTYYNPSL 84









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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 ; Search time 6.39091 Seconds  
(without alignments)  
838.855 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 ESEGGVLVPSQTLSTLCTV.....RSDGVLDMGQGLVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 440.5 | 71.7        | 129    | 1  | HV2F_HUMAN  |
| 2          | 417   | 67.9        | 146    | 1  | HV2F_HUMAN  |
| 3          | 381.5 | 62.1        | 117    | 1  | HV2G_HUMAN  |
| 4          | 363.5 | 59.2        | 137    | 1  | HV46_MOUSE  |
| 5          | 352.5 | 57.4        | 144    | 1  | HV43_MOUSE  |
| 6          | 347.5 | 56.6        | 113    | 1  | HV47_MOUSE  |
| 7          | 338.5 | 55.1        | 116    | 1  | HV61_MOUSE  |
| 8          | 335   | 54.6        | 117    | 1  | HV62_MOUSE  |
| 9          | 333.5 | 54.2        | 116    | 1  | HV60_MOUSE  |
| 10         | 325   | 52.9        | 135    | 1  | HV02_XENLA  |
| 11         | 314   | 51.1        | 120    | 1  | HV2B_HUMAN  |
| 12         | 295.5 | 48.1        | 119    | 1  | HV2C_HUMAN  |
| 13         | 294   | 47.9        | 147    | 1  | HV2H_HUMAN  |
| 14         | 288.5 | 47.0        | 136    | 1  | HV01_XENLA  |
| 15         | 288   | 46.9        | 115    | 1  | HV44_MOUSE  |
| 16         | 288   | 46.9        | 119    | 1  | HV40_MOUSE  |
| 17         | 287.5 | 46.8        | 125    | 1  | HV2D_HUMAN  |
| 18         | 286.5 | 46.7        | 121    | 1  | HV2E_HUMAN  |
| 19         | 285.5 | 46.5        | 117    | 1  | HV2B_RABIT  |
| 20         | 283   | 46.1        | 126    | 1  | HV2A_HUMAN  |
| 21         | 282   | 45.9        | 114    | 1  | HV3B_HUMAN  |
| 22         | 281   | 45.8        | 122    | 1  | HV3A_HUMAN  |
| 23         | 281   | 45.8        | 122    | 1  | HV3G_HUMAN  |
| 24         | 278   | 45.3        | 119    | 1  | HV37_MOUSE  |
| 25         | 277   | 45.1        | 116    | 1  | HV05_CARAU  |
| 26         | 276.5 | 45.0        | 121    | 1  | HV03_HUMAN  |
| 27         | 276   | 45.0        | 119    | 1  | HV38_MOUSE  |
| 28         | 275   | 44.8        | 116    | 1  | HV45_MOUSE  |
| 29         | 274.5 | 44.7        | 142    | 1  | HV01_XAT    |
| 30         | 274   | 44.6        | 136    | 1  | HV2C_RABIT  |
| 31         | 273.5 | 44.5        | 117    | 1  | HV41_MOUSE  |
| 32         | 273.5 | 44.5        | 117    | 1  | HV42_MOUSE  |
| 33         | 272   | 44.3        | 114    | 1  | HV2A_RABIT  |

|    |       |      |     |   |            |                     |
|----|-------|------|-----|---|------------|---------------------|
| 34 | 271   | 44.1 | 122 | 1 | HV3H_HUMAN | P01769 homo sapien  |
| 35 | 267   | 43.5 | 118 | 1 | HV51_MOUSE | P06330 mus musculus |
| 36 | 267   | 43.5 | 139 | 1 | HV07_MOUSE | P01751 mus musculus |
| 37 | 265.5 | 43.2 | 117 | 1 | HV12_MOUSE | P01756 mus musculus |
| 38 | 264.5 | 43.1 | 117 | 1 | HV3D_HUMAN | P01765 homo sapien  |
| 39 | 264.5 | 43.1 | 115 | 1 | HV13_MOUSE | P01757 mus musculus |
| 40 | 264   | 43.0 | 122 | 1 | HV20_MOUSE | P01789 mus musculus |
| 41 | 262.5 | 42.8 | 115 | 1 | HV3F_HUMAN | P01767 homo sapien  |
| 42 | 262.5 | 42.8 | 117 | 1 | HV02_CANPA | P01785 canis famill |
| 43 | 261   | 42.5 | 116 | 1 | HV3T_HUMAN | P01781 homo sapien  |
| 44 | 261   | 42.5 | 126 | 1 | HV3K_HUMAN | P01772 homo sapien  |
| 45 | 260   | 42.3 | 120 | 1 | HV50_MOUSE | P06329 mus musculus |

## ALIGNMENTS

## RESULT 1

ID HV2F\_HUMAN STANDARD; PRT; 129 AA.

AC P01824: 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region WAH.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.

RA MEDLINE=8222235; PubMed=6806818;  
RA Takahashi N., Tetaert D., Debure B., Lin L.-C., Putnam F.W.;  
RT "Complete amino acid sequence of the delta heavy chain of human  
immunoglobulin D."  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ISD MYELOMA  
PROTEIN.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02099; D2H0WA.  
DR HSSP; P01825; 7EAB.

DR GLCOSULTEDB; P01824; -  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG\_Like.  
DR InterPro; IPR003596; IG\_MHC.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGv\_1.

DR PROSITE; PS50835; IG\_Like; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 113 IG-LIKE.  
FT NON TER 129  
SQ SEQUENCE 129 AA; 14117 MW; DSD53D47ABES1319 CRC64;

Query Match 71.7%; Score 440.5; DB 1; Length 129;  
Best Local Similarity 65.1%; Pred. No. 2.1e-38;  
Matches 82; Conservative 14; Mismatches 15; Indels 15; Gaps 2;

|    |     |   |     |
|----|-----|---|-----|
| QY | 2   | ESGPGVLVPSQTLSTLCTVSGSIRSGGYSWVRQPGKGLGEMIGNIYHSGNTYNSL | 61  |
| DB | 6   | ESGPGVLVPSQTLSTLCTVSGSIRSGGYSWVRQPGKGLGEMIGNIYHSGNTYNSL | 65  |
| QY | 62  | KSRTMSVDSKKNFSLISVTADTAIVYCAR                           | 108 |
| DB | 66  | RGRTVISTDSRNQPSLIRMSAADTAMYYCAGNPPYYDITGSDG--IDWGGGT    | 123 |
| QY | 109 | LVTVSS 114  |     |
| DB | 124 | TVHVS 129   |     |

RESULT 2  
 HV21 HUMAN STANDARD; PRT; 146 AA.  
 ID HV21 HUMAN  
 AC P06331;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-II region ARH-77 precursor.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85205332; PubMed=3922855;  
 RA Kudo A., Ishihara T., Nishimura Y., Matanabe T.;  
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-  
 RT repeat sequence in 5' flanking region.";  
 RL Gene 33:181-189 (1985).  
 DR PIR; A02101; GIHUR2.  
 DR HSSP; P01825; 7FAB.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT CHAIN 1 19  
 FT DOMAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.  
 FT DOMAIN 20 117 V SEGMENT.  
 FT DOMAIN 118 127 D SEGMENT.  
 FT DOMAIN 128 146 J SEGMENT.  
 FT DISULFID 42 115 BY SIMILARITY.  
 FT NON\_TER 146 146  
 SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218117F CRC64;  
 Query Match 67.9%; Score 417; DB 1; Length 146;  
 Best Local Similarity 68.6%; Pred. No. 6, 2e-36;  
 Matches 83; Conservative 10; Mismatches 16; Indels 12; Gaps 3;  
 QY 4 GPGLVKPSQTLSTCTVSGSGSIRSGYMSWRQPEKGLWIGNTYHSNTYNSPLK 63  
 DB 28 GAGLVKPSQTLSTCTVSGSGSIRSGYMSWRQPEKGLWIGNTYHSNTYNSPLK 85  
 QY 64 RITMSVDTSKNHFSLRTSYTAADTAAYYCARG--DG-----YTLDNWGGGLTYVS 113  
 DB 86 RVTISLDTSKNHFSLRTSYTAADTAAYYCARGLLRGWMDVDYYIGMDVWGGSITVTVS 145  
 QY 114 S 114  
 DB 146 S 146  
 RESULT 3  
 HV2G HUMAN STANDARD; PRT; 117 AA.  
 ID HV2G HUMAN  
 AC P01835;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region NEMM.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77242302; PubMed=407927;  
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;

RT "Amino acid sequence of the VH region of a human myeloma  
 RT immunoglobulin (Ig New)."  
 RT Biochemistry 16:3412-3420 (1977).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.  
 RX MEDLINE=78066916; PubMed=618887;  
 RA Saul F.A., Amzel L.M., Poljak R.J.;  
 RT "Preliminary refinement and structural analysis of the Fab fragment  
 RT from human immunoglobulin new at 2.0-A resolution.";  
 RL J. Biol. Chem. 253:585-597 (1978).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 CC PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A90404; GIHUM.  
 DR PDB; 7FAB; 31-JAN-94.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR PIR; A02101; GIHUR2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 111  
 FT MOD\_RES 1 111  
 FT STRAND 3 7  
 FT STRAND 11 12  
 FT TURN 14 15  
 FT STRAND 18 25  
 FT TURN 30 31  
 FT STRAND 33 39  
 FT TURN 41 42  
 FT STRAND 46 51  
 FT TURN 53 54  
 FT STRAND 57 59  
 FT HELIX 61 63  
 FT TURN 64 66  
 FT STRAND 67 72  
 FT TURN 73 76  
 FT STRAND 77 82  
 FT HELIX 87 89  
 FT STRAND 91 98  
 FT STRAND 104 107  
 FT STRAND 111 115  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;  
 Query Match 62.1%; Score 381.5; DB 1; Length 117;  
 Best Local Similarity 65.8%; Pred. No. 2, 2e-32;  
 Matches 75; Conservative 17; Mismatches 19; Indels 3; Gaps 2;  
 QY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGYMSWRQPEKGLWIGNTYNSPL 61  
 DB 6 QSGPGLVPSQTLSTCTVSGSGSIRSGYMSWRQPEKGLWIGNTYNSPL 63  
 QY 62 KSRITMSVDTSKNHFSLRTSYTAADTAAYYCARG--DGTYTLDNWGGGLTYVS 114  
 DB 64 RSRVTMLVDTSKNHFSLRTSYTAADTAAYYCARGLLRGWMDVDYYIGMDVWGGSITVTVS 117  
 RESULT 4  
 HV46 MOUSE STANDARD; PRT; 137 AA.  
 ID HV46 MOUSE  
 AC P01832;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig heavy chain V region MOPC 315 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=89238351; PubMed=2497341;  
 RA Riffert A., Horne C., Dorrington K.J., Klein M.;  
 RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH  
 gene segment";  
 RL Mol. Immunol. 26:431-434 (1989).  
 RN [2]  
 RN SEQUENCE OF 1-31.  
 RX MEDLINE=78094475; PubMed=414225;  
 RA Jilka R.L., Pestka S.;  
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse  
 immunoglobulin heavy chain";  
 RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).  
 RN [3]  
 RN SEQUENCE OF 1-21.  
 RX MEDLINE=79148758; PubMed=428562;  
 RA Schechter I., Wolf O., Zemell R., Burstein Y.;  
 RT "Structure and function of immunoglobulin genes and precursors";  
 RL Fed. Proc. 38:1839-1845 (1979).  
 RN [4]  
 RN SEQUENCE OF 19-136.  
 RX MEDLINE=74170779; PubMed=4524622;  
 RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;  
 RT "Amino-acid sequence of the variable region of the heavy (alpha)  
 chain of a mouse myeloma protein with anti-hapten activity";  
 RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).  
 RN [5]  
 RN REVISION TO 53.  
 RX MEDLINE=77244979; PubMed=268248;  
 RA Hood L., Margolies M.N., Givol D., Zakut R.;  
 RL Unpublished results, cited by:  
 RL Padlan E.A., Davies D.R., Peck I., Givol D., Wright C.;  
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).  
 CC -I- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA  
 PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.  
 CC -----  
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 CC -----  
 DR EMBL; M27638; AAA61337.1; -;  
 DR EMBL; X07880; CAA30727.1; -;  
 DR PIR; P01825; AYMS35.  
 DR HSP; P01825; 7FAB.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.  
 FT DOMAIN 19 48 FRAMEWORK-1.  
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 85 116 FRAMEWORK-3.  
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 127 137 FRAMEWORK-4.  
 FT DISULFID 40 114 BY SIMILARITY.  
 FT CONFLICT 15 15 G-> GG (IN REF. 1; CAA30727).  
 FT CONFLICT 15 15 G-> H (IN REF. 2).  
 FT CONFLICT 77 78 GY-> YG (IN REF. 4).  
 FT CONFLICT 102 102 N-> D (IN REF. 4).  
 FT CONFLICT 123 123 MISSING (IN REF. 4).  
 FT NON\_TER 137 137

SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;  
 Query Match 59.2%; Score 363.5; DB 1; Length 137;  
 Best Local Similarity 60.9%; Pred. No. 1.8e-30;  
 Matches 70; Conservative 18; Mismatches 24; Indels 3; Gaps 2;  
 Oy 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYVSWRPGKGLIEMIGNIYHSGNTYVPSL 61  
 Db 24 ESGPGLVPSQTLSTCTVSGSGSIRSGGYVSWRPGKGLIEMIGNIYHSGNTYVPSL 82  
 Oy 62 KSRITMSVDTSKNPSRLTSVTADPAVYVCASDGC--YTLDNWGQGLTVVSS 114  
 Db 83 KNRVSIPTDTSNQFLKINSVTTEDPATYTCAGDNHLLYFDYWGQGLTVVSS 137  
 RESULT 5  
 ID HV43 MOUSE STANDARD; PRT; 144 AA.  
 AC P01819;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region MOPC 141 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=81012133; PubMed=6774258;  
 RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;  
 RT "Two types of somatic recombination are necessary for the generation  
 of complete immunoglobulin heavy-chain genes";  
 RL Nature 286:676-683 (1980).  
 CC -I- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A  
 CC DIFFERENTIAL GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.  
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; V00768; CAA24149.1; -;  
 DR PIR; A02094; G2MS14.  
 DR HSP; P01825; 7FAB.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.  
 FT DOMAIN 20 130 IG-LIKE.  
 FT NON\_TER 144 144  
 SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;  
 Query Match 57.4%; Score 352.5; DB 1; Length 144;  
 Best Local Similarity 59.8%; Pred. No. 2.6e-29;  
 Matches 73; Conservative 16; Mismatches 22; Indels 11; Gaps 3;  
 Oy 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYVSWRPGKGLIEMIGNIYHSGNTYVPSL 61  
 Db 25 ESGPGLVPSQTLSTCTVSGSGSLT--GYGNWVRQPGKGLIEMIGNIYHSGNTYVPSL 82  
 Oy 62 KSRITMSVDTSKNPSRLTSVTADPAVYVCA-----RSDGY-TLDNWGQGLTVTV 112  
 Db 83 KSRITITDNRKSGVFLKMSNLQTDITARYYCAVSIIYYRSDKXFLTDYWGQGLTVTV 142

QY 113 SS 114  
113 SS 114  
Db 143 SS 144

## RESULT 6

HV47\_MOUSE STANDARD; PRT; 113 AA.  
ID HV47\_MOUSE  
AC P01823;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 36-60.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;

CC [1]  
CC STRAIN=A/J;  
CC MEDLINE=84024551; PubMed=6414509;  
CC Juszczak E.C., Margolies M.N.;  
CC "Amino acid sequence of the heavy chain variable region from the A/J  
RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor  
RT idioType."  
RT IdioType."  
RT Biochemistry 22:4291-4296(1983).  
RL -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTARSONATE  
CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND  
CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTARSONATE RESPONSE OF  
CC STRAIN A/J MICE.

CC PIR; A02098; GMS60.  
CC PDB; 1J10; 18-FEB-03.  
CC PDB; 1J1X; 18-FEB-03.  
CC InterPro: IPR007110; IG-like.  
CC InterPro: IPR003006; IG\_MHC.  
CC InterPro: IPR003596; IG\_V.  
CC Pfam; PF00047; IG\_V.1.  
CC SMART; SM00406; IGV.1.  
CC PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT NON TER 113  
SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0B3F507B7 CRC64;

Query Match 56.6%; Score 347.5; DB 1; Length 113;  
Best Local Similarity 61.9%; Pred. No. 6.4e-29;  
Matches 70; Conservative 15; Mismatches 23; Indels 5; Gaps 2;

QY 2 EESGPGLVKPSQTLSTCTVSGSGSIRSGGYWVWVQPPGKGLWIGNIYHSGNTYNNPSL 61  
DB 6 EESGPGLVKPSQTLSTCTVSGSGSIRSGGYWVWVQPPGKGLWIGNIYHSGNTYNNPSL 63  
DB 64 KSRITSDTDSKNQFSLRLTSVTAADTAAYVYCARSDGYTLDMNGGTLVTVSS 114  
DB 64 KSRITSDTDSKNQFSLRLTSVTAADTAAYVYCARSDGYTLDMNGGTLVTVSS 113

## RESULT 7

HV61\_MOUSE STANDARD; PRT; 116 AA.  
ID HV61\_MOUSE  
AC P18532;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 1B43 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/CJ;

RX MEDLINE=89279149; PubMed=2499654;  
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during  
RT the primary immune response."  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.  
CC PIR; J0508; HVM51B.  
DR PDB; 1KCS; 11-MAY-02.  
DR PDB; 1KCV; 11-MAY-02.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam; PF00047; IGV.1.  
DR SMART; SM00406; IGV.1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal; 3D-structure.

FT SIGNAL 1 18  
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.  
FT DOMAIN 19 48 FRAMEWORK-1.  
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 54 67 FRAMEWORK-2.  
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 85 116 FRAMEWORK-3.  
FT DISULFID 40 114 BY SIMILARITY.  
FT NON TER 116  
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681PF74 CRC64;

Query Match 55.1%; Score 338.5; DB 1; Length 116;  
Best Local Similarity 70.2%; Pred. No. 5.5e-28;  
Matches 66; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

QY 2 EESGPGLVKPSQTLSTCTVSGSGSIRSGGYWVWVQPPGKGLWIGNIYHSGNTYNNPSL 61  
DB 24 EESGPGLVKPSQTLSTCTVSGSGSIRSGGYWVWVQPPGKGLWIGNIYHSGNTYNNPSL 82  
QY 62 KSRITSDTDSKNQFSLRLTSVTAADTAAYVYCAR 95  
DB 83 KSRITSDTDSKNQFSLRLTSVTAADTAAYVYCAR 116

## RESULT 8

HV62\_MOUSE STANDARD; PRT; 117 AA.  
ID HV62\_MOUSE  
AC P18533;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 733 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/CJ;  
RX MEDLINE=89279149; PubMed=2499654;  
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during  
RT the primary immune response."  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC PIR; J0510; HVM573.  
DR HSSP; P01825; 7EAB.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam; PF00047; IGV.1.  
DR SMART; SM00406; IGV.1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.  
FT DOMAIN 19 >117 IG-LIKE.

```

AC P20957; (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager U., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains."
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
RL -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J03632; AAA49791.1; -.
CC PIR; B31933; B31933.
CC HSP; P01810; 2PBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IgV; 1.
CC PROSITE; PSS0835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
KW IMUNOTER 1
FT SIGNAL 1
FT CHAIN 19 18 IG HEAVY CHAIN V REGION XIG14.
FT DOMAIN 20 128 IG-LIKE.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; B6C467105C00732E CRC64;

Query March 52.9%; Score 325; DB 1; Length 135;
Best Local Similarity 54.8%; Pred. No. 1,66-26;
Matches 63; Conservative 17; Mismatches 31; Indels 4; Gaps 2;

QY 2 ESGGGLVPSQTLSLNCTVSGGSIIRSGGYWVRQPPGKLEIMIGNIYHSGNTYNPSTL 61
DB 23 ESGGGTVKPSBSRLTCTVSGFELSS--YHWHWIRQPPGKLEWIGVIATGSGTAIDSL 80
QY 62 KSRITMSVDRISKHFSLRLTSVTRADPAVNYCAR--SDGTLLDWGGGTLTVTVSS 114
DB 81 KNRVTITKDKGKKQVYLQNNGMVEYKDTAMYYCAREYASGYNFWDVGGTMTVTVTS 135

RESULT 11
ID HV2B_HUMAN STANDARD; PRT; 120 AA.
AC P01815;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region COR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
```

RA Prese E.M., Hogg N.M.;  
RT "The amino acid sequences of the Fd fragments of two human gamma-1  
heavy chains";  
RL Biochem. J. 117:641-660(1970).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
PROTEIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR: A02089; G1HUCO.  
DR HSSP: P01825; 7FAB.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.  
FT MOD RES 1 110  
FT DISULFID 22 94  
FT CARBOHYD 62 62  
FT NON TER 120 120  
SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EB98 CRC64;  
Query Match 51.1%; Score 314; DB 1; Length 120;  
Best Local Similarity 55.5%; Pred. No. 1,9e-25;  
Matches 66; Conservative 14; Mismatches 29; Indels 10; Gaps 3;  
QY 2 ESGPGIVKPSQTLSTCTVSGSIRSGYMSWVOPPGKGLMIGNIYHSGNTYYNPSL 61  
DB 6 ESGPALVKPTQTLTLCTFSGSLSGTCMVCVMIRQDPGKLEMLARIDMDKTYGASL 65  
66 ETRLTISKTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 120  
QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCAR-----SDGYTLDMNGQGLTVYSS 114  
DB 66 ETRLTISKTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 120  
RESULT 12  
ID HV2H HUMAN STANDARD; PRT; 119 AA.  
AC P01816;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG heavy chain V-II region DM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=70258837; PubMed=5449120;  
RA Prese E.M., Hogg N.M.;  
RT "The amino acid sequences of the Fd fragments of two human gamma-1  
heavy chains";  
RL Biochem. J. 117:641-660(1970).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE  
SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR: A02091; G1HUCP.  
DR HSSP: P01789; 1MCP.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Pyrrolidone carboxylic acid.

FT DOMAIN 1 113  
FT MOD RES 1 1  
FT NON TER 119 119  
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;  
Query Match 48.1%; Score 295.5; DB 1; Length 119;  
Best Local Similarity 52.6%; Pred. No. 1.5e-23;  
Matches 60; Conservative 16; Mismatches 37; Indels 1; Gaps 1;  
QY 2 ESGPGIVKPSQTLSTCTVSGSIRSGYMSWVOPPGKGLMIGNIYHSGNTYYNPSL 61  
DB 6 ESGPALVKPTQTLTLCTFSGSLSGTCMVCVMIRQDPGKLEMLARIDMDKTYGASL 65  
66 ETRLTISKTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 119  
QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCARSDG---YTLDMNGQGLTVYSS 114  
DB 66 ETRLTISKTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 119  
RESULT 13  
ID HV2H HUMAN STANDARD; PRT; 147 AA.  
AC P04358;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG heavy chain V-II region SSS precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84298107; PubMed=6089186;  
RA Takashi N., Noma T., Honjo T.;  
RT "Rearranged immunoglobulin heavy chain variable region (VH)  
pseudogene that deletes the second complementarity-determining  
region";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).  
DR PIR: A02090; G2HUCS.  
DR HSSP: P01825; 7FAB.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 147  
FT DOMAIN 20 118  
FT DOMAIN 119 132  
FT DOMAIN 133 147  
FT NON TER 147 147  
SQ SEQUENCE 147 AA; 16323 MW; FCBDB3D00FB666 CRC64;  
Query Match 47.9%; Score 294; DB 1; Length 147;  
Best Local Similarity 49.6%; Pred. No. 2.7e-23;  
Matches 58; Conservative 15; Mismatches 34; Indels 10; Gaps 1;  
QY 2 ESGPGIVKPSQTLSTCTVSGSIRSGYMSWVOPPGKGLMIGNIYHSGNTYYNPSL 61  
DB 25 ESGPALVKPTQTLTLCTFSGSLSVNTRGNSVWIRQDPGKLEMLARIDMDKTYGASL 84  
62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCARSD-----GYTLDMNGQGLTVYSS 108  
DB 85 ETRLTISKTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 141  
RESULT 14  
HV01\_XENLA



```

ID HV01_XENLA STANDARD; PRT; 136 AA.
AC P20956;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG8 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Fipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; Pubmed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains."
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -i- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M20484; AAA49774.1; ALT_TERM.
DR PIR; A31933; A31933.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19 136 IG HEAVY CHAIN V REGION XIG8.
FT DOMAIN 19 128 IG-LIKE.
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15123 MW; 3141838981441963 CRC64;

Query Match
Best Local Similarity 47.0%; Score 288.5; DB 1; Length 136;
Matches 59; Conservative 19; Mismatches 32; Indels 7; Gaps 3;

QY 2 ESGPGLVRSQTLSTCTVSGSIRSGGYMSWROPGKGLMIGNIYHSGNTYYNPSL 61
DB 23 ESGPGLVRSQTLSTCTVSGSIRSGGYMSWROPGKGLMIGNIYHSGNTYYNPSL 61
QY 62 KSRITMSVDTSKMFSLRLTSTADTARYYC-----ARSDGTLDDWGCGTLVYVSS 114
DB 81 KNRVTITDNGKKQYVLTQNNMEVVDXTANYCTSTLAGAGY-FEHMGQITVYVTS 136

RESULT 15
HV44_MOUSE STANDARD; PRT; 115 AA.
ID HV44_MOUSE
AC P01820;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region P14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=81012133; Pubmed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC -i- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00767; CAA24148.1; -.
DR PIR; A02095; HVMS14.
DR PDB; 1A7N; 29-APR-98.
DR PDB; 1A7O; 29-APR-98.
DR PDB; 1A7P; 29-APR-98.
DR PDB; 1A7R; 29-APR-98.
DR PDB; 1G7H; 17-JAN-01.
DR PDB; 1G7I; 17-JAN-01.
DR PDB; 1G7J; 17-JAN-01.
DR PDB; 1G7M; 17-JAN-01.
DR PDB; 43C9; 24-JUL-02.
DR PDB; 43CA; 24-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1
FT CHAIN 19 115 IG HEAVY CHAIN V REGION P14.
FT DOMAIN 20 >115 IG-LIKE.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;

Query Match
Best Local Similarity 46.9%; Score 288; DB 1; Length 115;
Matches 56; Conservative 15; Mismatches 20; Indels 2; Gaps 1;

QY 2 ESGPGLVRSQTLSTCTVSGSIRSGGYMSWROPGKGLMIGNIYHSGNTYYNPSL 61
DB 25 ESGPGLVRSQTLSTCTVSGSIRSGGYMSWROPGKGLMIGNIYHSGNTYYNPSL 61
QY 62 KSRITMSVDTSKMFSLRLTSTADTARYYC-----ARSDGTLDDWGCGTLVYVSS 114
DB 83 KSRITMSVDTSKMFSLRLTSTADTARYYC-----ARSDGTLDDWGCGTLVYVSS 114

Search completed: February 10, 2004, 18:36:30
Job time : 7.39091 secs

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[illegible]

Db 25 ESGPGLVPSKPSLSTLCTVSGSGSSSTNYWGMIRQPEKGLWIGSLHNHSGSDYNNPSL 84  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSGYTLDMNGGTLVTYSS 114  
 85 KSRVITISVDTSKNQPSLRLTSVTAADTAAYVYCARLGMGAFDFGHTMTYSS 137

## RESULT 2

Q96KX8 PRELIMINARY; PRT; 496 AA.  
 ID Q96KX8  
 AC Q96KX8; 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC016369; AAI16369.1; -  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 4.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 4.  
 DR PROSITE: PSS0290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 496 AA; 53391 MW; D34692984904069 CRC64;

Query Match 75.9%; Score 466; DB 4; Length 496;  
 Best Local Similarity 74.2%; Pred. No. 1.2e-40;  
 Matches 89; Conservative 10; Mismatches 13; Indels 8; Gaps 2;

QY 2 ESGPGLVPSKPSLSTLCTVSGSGSSIRSGGYWVWVQPPGKGLWIGNTYHSGNTYNNPSL 61  
 25 ESGPGLVPSKPSLSTLCTVSGSGSSIRSGGYWVWVQPPGKGLWIGNTYHSGNTYNNPSL 84  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSGDYT-----LDMNGGTLVTYSS 114  
 85 KSRVITISVDTSKNQPSLRLTSVTAADTAAYVYCAR-HGYSKSGRTGALDIWGGTLVTYSS 143

## RESULT 3

Q9UL73 PRELIMINARY; PRT; 119 AA.  
 ID Q9UL73  
 AC Q9UL73; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M., Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 CLin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035041; AAD56277.1; -  
 DR HSP; P01825; 7PAB.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 119 119  
 SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA0BE CRC64;

Query Match 75.5%; Score 463.5; DB 4; Length 119;  
 Best Local Similarity 77.6%; Pred. No. 3.8e-41;  
 Matches 90; Conservative 9; Mismatches 12; Indels 5; Gaps 2;

QY 2 ESGPGLVPSKPSLSTLCTVSGSGSSIRSGGYWVWVQPPGKGLWIGNTYHSGNTYNNPSL 61  
 Db 6 ESGPGLVPSKPSLSTLCTVSGSGSSIRSGGYWVWVQPPGKGLWIGNTYHSGNTYNNPSL 63  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDG---YTLDMNGGTLVTYSS 114  
 Db 64 KSRVITISVDTSKNQPSLRLTSVTAADTAAYVYCARLSMNGPYFDYWGQTLVTYSS 119

## RESULT 4

Q96EYO PRELIMINARY; PRT; 613 AA.  
 ID Q96EYO  
 AC Q96EYO; 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC011857; AAI11857.1; -  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 5.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 5.  
 DR PROSITE: PSS0290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 74.4%; Score 457; DB 4; Length 613;  
 Best Local Similarity 78.0%; Pred. No. 1.4e-39;  
 Matches 92; Conservative 7; Mismatches 11; Indels 8; Gaps 3;

QY 2 ESGPGLVPSKPSLSTLCTVSGSGSSIRSGGYWVWVQPPGKGLWIGNTYHSGNTYNNPSL 61  
 25 ESGPGLVPSKPSLSTLCTVSGSGSSIRSGGYWVWVQPPGKGLWIGNTYHSGNTYNNPSL 82  
 Db 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDGTLDN-----WGQTLVTYSS 114  
 83 KSRVITISVDTSKNQPSLRLTSVTAADTAAYVYCAR-SQPWELPTVGLFYWGQTLVTYSS 139

## RESULT 5

Q81ZD7 PRELIMINARY; PRT; 130 AA.  
 ID Q81ZD7  
 AC Q81ZD7; 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anti-thyroglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

```

OX NCB1_TaxID=9606;
RN SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RT "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
  Throglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145445; AAN64329.1; -.
FT NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6ECC1551E CRC64;

Query Match 69.5%; Score 429; DB 4; Length 130;
Best Local Similarity 68.8%; Pred. No. 1.8e-37;
Matches 86; Conservative 12; Mismatches 15; Indels 12; Gaps 4;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPFGKLEWIGNIYHSGNT-----Y 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 6 QSGPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPFGKLEWIGNIYHSGNTYSGSPY 65

QY 57 YNPSLKSRTITMSVDTSKNHFSLRLSVTAADTAAYYCAR-----SDG--YT-LDNWGQGLT 109
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 66 YAPSLRSRVIIISVDTSKQLSLRLSSVTAADTAAYYCARPTHCSSGCGYAFQHWGQGL 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 110 VTWSS 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 126 VTWSS 130
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FCG0DBAD82B39FD7 CRC64;

Query Match 69.5%; Score 426.5; DB 4; Length 588;
Best Local Similarity 70.0%; Pred. No. 2.2e-36;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPFGKLEWIGNIYHSGNTYHNSPLKS 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 27 GAGLKPSETLSTCTGVYGSF--SGYWSWIRPPGKLEWIGIHNHSGSTYHNSPLKS 84

QY 64 RTTMSVDTSKNHFSLRLSVTAADTAAYYCAR-----SDG--YT-LDNWGQGLT 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 85 RVTISVDTSKQLSLRLSSVTAADTAAYYCARVITRASPGTDGRYGMVWGQGLTVYSS 144
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q9BU10 PRELIMINARY; PRT; 597 AA.

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AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSPD; P01825; FRAB.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8F87E055851 CRC64;

Query Match 69.5%; Score 426.5; DB 4; Length 597;
Best Local Similarity 70.0%; Pred. No. 2.2e-36;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPFGKLEWIGNIYHSGNTYHNSPLKS 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 27 GAGLKPSETLSTCTGVYGSF--SGYWSWIRPPGKLEWIGIHNHSGSTYHNSPLKS 84

QY 64 RTTMSVDTSKNHFSLRLSVTAADTAAYYCAR-----SDG--YT-LDNWGQGLT 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 85 RVTISVDTSKQLSLRLSSVTAADTAAYYCARVITRASPGTDGRYGMVWGQGLTVYSS 144
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q96AA6 PRELIMINARY; PRT; 618 AA.
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 69.5%; Score 426.5; DB 4; Length 618;
Best Local Similarity 70.0%; Pred. No. 2.3e-36;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPFGKLEWIGNIYHSGNTYHNSPLKS 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 27 GAGLKPSETLSLTCGVGGSF--SGYWSMIRQPGKLEWIGELINHSNSTYNSLS 84  
 QY 64 RITMSVDTSKNHSLSLTSTVTAADTAIVYICAR-----SDG-YTLDMWGQTLVTSS 114  
 Db 85 RVTISVDTSKKQLSLKLSVNAADTAIVYICARVITRASPGTDGRYGMVWGQGTIVTVSS 144

## RESULT 9

Q9BOB8 ID Q9BOB8 PRELIMINARY; PRT; 597 AA.

AC 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle, and Lymph;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC006180; AAH06180.1; -  
 DR EMBL; BC001872; AAH01872.1; -  
 DR HSSP; P01825; 7PAB.  
 DR InterPro; IPR007110; Ig-1ike.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 68.8%; Score 422.5; DB 4; Length 597;  
 Best Local Similarity 70.0%; Pred. No. 5.8e-36;  
 Matches 84; Conservative 9; Mismatches 16; Indels 11; Gaps 3;

QY 4 GPGVLKPSQTLSTCTVSGGSGIRSGYWSWVRQPGKLEWIGELINHSNSTYNSLS 63  
 Db 27 GAGLKPSETLSLTCGVGGSF--SGYWSMIRQPGKLEWIGELINHSNSTYNSLS 84  
 QY 64 RITMSVDTSKNHSLSLTSTVTAADTAIVYICAR-----SDG-YTLDMWGQTLVTSS 114  
 Db 85 RVTISVDTSKKQLSLKLSVNAADTAIVYICARVITRASPGTDGRYGMVWGQGTIVTVSS 144

## RESULT 10

Q8TC63 ID Q8TC63 PRELIMINARY; PRT; 473 AA.

AC 08TC63;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025985; AAH25985.1; -  
 DR InterPro; IPR000923; BlueCu\_1.  
 DR InterPro; IPR007110; Ig-1ike.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 Pfam; PF00047; Ig; 4.

DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00196; COPPER BLUE; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 67.3%; Score 413; DB 4; Length 473;  
 Best Local Similarity 69.0%; Pred. No. 4.4e-35;  
 Matches 80; Conservative 11; Mismatches 15; Indels 6; Gaps 2;

QY 2 ESGPGLKPSQTLSTCTVSGGSGIRSGYWSWVRQPGKLEWIGELINHSNSTYNSLS 61  
 Db 32 ESGPGLKPSQTLSTCTVSGGSGIRSGYWSWVRQPGKLEWIGELINHSNSTYNSLS 91  
 QY 62 KSRITMSVDTSKNHSLSLTSTVTAADTAIVYICARBDGTL---DNMGQTLVTSS 113  
 Db 92 RSRVTMSADMSNSPYLKLSVTAADTAIVYICAA--GHLVWGFGAHWGQGLVSVS 145

## RESULT 11

Q99M22 ID Q99M22 PRELIMINARY; PRT; 479 AA.

AC 099M22;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical 52.0 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002091; AAH02091.1; -  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig-1ike.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 62.3%; Score 382.5; DB 11; Length 479;  
 Best Local Similarity 66.7%; Pred. No. 7.2e-32;  
 Matches 76; Conservative 15; Mismatches 20; Indels 3; Gaps 3;

QY 2 ESGPGLKPSQTLSTCTVSGGSGIRSGYWSWVRQPGKLEWIGELINHSNSTYNSLS 61  
 Db 24 ESGPGLKPSQTLSTCTVSGGSGIRSGYWSWVRQPGKLEWIGELINHSNSTYNSLS 82  
 QY 62 KSRITMSVDTSKNHSLSLTSTVTAADTAIVYICARBDGTL---DNMGQTLVTSS 114  
 Db 83 KSRITMSVDTSKNHSLSLTSTVTAADTAIVYICARBDGTL---DNMGQTLVTSS 135

## RESULT 12

Q9UL75 ID Q9UL75 PRELIMINARY; PRT; 122 AA.

AC 09UL75;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
  Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL, AF035039; AAD56275.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match 59.4%; Score 365; DB 4; Length 122;
Best Local Similarity 61.5%; Pred. No. 9.2e-31;
Matches 72; Conservative 12; Mismatches 29; Indels 4; Gaps 2;

Qy 2 ESGPGLVAPSGTSLTCTVSGSGSIRSGYMSWVRQPPKGLGEMWIGNIYHSGNTY--YNP 59
Db 6 QSGPGLVAPSGTSLTCAISGDSVSSNSAMWIKQSPRGLEWIGRTYRSKMYNDYRV 65

Qy 60 SLKSRITMSVDTSKNHFSLRLTSVTADPAVYVCARSDGY--TLNMGCGTLVTVSS 114
Db 66 SVKSRITINPTSKQFSLQINSVTPEDTAVYVCARDLELGGFYMGGTLVTVSS 122

RESULT 13
Q9UL96 PRELIMINARY; PRT; 121 AA.
AC Q9UL96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
  (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
  Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL, AF035018; AAD56254.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 56.4%; Score 346.5; DB 4; Length 121;
Best Local Similarity 58.6%; Pred. No. 8.1e-29;
Matches 68; Conservative 13; Mismatches 32; Indels 3; Gaps 1;

Qy 2 ESGPGLVAPSGTSLTCTVSGSGSIRSGYMSWVRQPPKGLGEMWIGNIYHSGNTYNP 61
Db 2 ESGPGLVAPSGTSLTCTVSGSGSIRSGYMSWVRQPPKGLGEMWIGNIYHSGNTYNP 61

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Db 6 ESGPGLVAPSGTSLTCTVSGSGSIRSGMDVWIRQPPKGLALEWIALIYWD DKRYSPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTADPAVYVCAR---SDGYTLNMGCGTLVTVSS 114
Db 66 KSRITITKDTSKNOVDLTMTWMDPMDTATVYCAHRKSGDGYFDYMGCGTLVTVSS 121

RESULT 14
Q99NG4 PRELIMINARY; PRT; 121 AA.
AC Q99NG4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Placental PHENI.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
  Bautsch W., Kola A., Kios A., Koehl J.;
RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries";
RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Placental.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;

Query Match 55.2%; Score 339; DB 11; Length 121;
Best Local Similarity 59.0%; Pred. No. 5e-28;
Matches 69; Conservative 14; Mismatches 28; Indels 6; Gaps 2;

Qy 2 ESGPGLVAPSGTSLTCTVSGSGSIRSGYMSWVRQPPKGLGEMWIGNIYHSGNTYNP 61
Db 6 ESGPGLVAPSGTSLTCTVSGSGFPLTSHGV--SWVRQPPKGLGEMWIGVMDGNTKYHSL 63

Qy 62 KSRITMSVDTSKNHFSLRLTSVTADPAVYVCARS---DEYTLNMGCGTLVTVSS 114
Db 64 ISRLSISKNSKSOVFLKLSLQTEDTATVYCAHRYRYKANYAMDYMGSGTVSS 120

RESULT 15
Q91X92 PRELIMINARY; PRT; 482 AA.
AC Q91X92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown (protein for MGC:18822).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL EMBL; BC011181; AAH1181.1; -.
DR InterPro; IPR007110; IG_1like.

```

DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF0047; IG\_4.  
DR SMART: SM00406; IG\_1.  
DR PROSITE: PS00835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; 2.  
SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;

Query Match 54.6%; Score 335; DB 11; Length 482;  
Best Local Similarity 59.1%; Pred. No. 7.3e-27;  
Matches 68; Conservative 15; Mismatches 28; Indels 4; Gaps 2;

|    |    |   |     |
|----|----|---|-----|
| Qy | 2  | ESGPGIWKPSQTLSTCTVSGGSIKSGYVWVROPFGKLEWIGNIYHSGNTYYNPSL | 61  |
| Db | 25 | ESGPDIVAPSQSLITCTVSGFALTS--YAIWVROPPGKLEWLVITGCVTNYNSAL | 82  |
| Qy | 62 | KSRIWSDVTSKNHFSRLTSVTAADTAVYYCARSDGY--TLDNMGQTLVTYSS    | 114 |
| Db | 83 | KSRLSISKNSKSGQVFLKNNSLQTNLTARYYCARSDNTEGAMDYWGQTSVTYSS  | 137 |

Search completed: February 10, 2004, 18:39:20  
Job time : 26.9455 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 11.7455 Seconds

(without alignments)  
933.402 Million cell updates/sec

Title: US-10-027-725A-9

Sequence: 1 LBSGPGLVKPSQTLSTCTV.....RSDGYTLDMNGQGLTVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 501.5 | 81.7        | 135    | 2 S78051 | Ig heavy chain pre |
| 2          | 497.5 | 81.0        | 147    | 2 S13519 | Ig heavy chain V r |
| 3          | 492.5 | 80.2        | 140    | 2 I37782 | Ig variable region |
| 4          | 490   | 79.8        | 130    | 2 S30534 | Ig heavy chain V r |
| 5          | 488.5 | 79.6        | 116    | 2 S37456 | Ig mu chain - huma |
| 6          | 487.5 | 79.4        | 130    | 2 S31690 | Ig heavy chain V r |
| 7          | 480.5 | 78.3        | 121    | 2 S44113 | Ig heavy chain V r |
| 8          | 479.5 | 78.1        | 155    | 2 S31511 | Ig heavy chain - h |
| 9          | 477.5 | 77.8        | 146    | 2 S09710 | Ig heavy chain V r |
| 10         | 477.5 | 77.8        | 155    | 2 S31512 | Ig heavy chain - h |
| 11         | 473.5 | 77.1        | 146    | 2 S09711 | Ig heavy chain V r |
| 12         | 472.5 | 77.0        | 127    | 2 S19668 | Ig heavy chain V r |
| 13         | 472.5 | 77.0        | 128    | 2 S31514 | Ig heavy chain - h |
| 14         | 472   | 76.9        | 137    | 2 S26803 | Ig heavy chain V r |
| 15         | 469   | 76.4        | 99     | 2 S26803 | Ig heavy chain V r |
| 16         | 467.5 | 76.1        | 123    | 2 S30530 | Ig heavy chain V r |
| 17         | 467   | 76.1        | 99     | 2 S26801 | Ig heavy chain V r |
| 18         | 467   | 76.1        | 122    | 2 S69912 | Ig V-D-J region (N |
| 19         | 465   | 75.7        | 139    | 2 S31586 | Ig heavy chain V r |
| 20         | 464   | 75.6        | 99     | 2 S26802 | Ig heavy chain V r |
| 21         | 461   | 75.1        | 145    | 2 S78055 | Ig heavy chain pre |
| 22         | 460.5 | 75.0        | 109    | 2 PH1673 | Ig heavy chain V r |
| 23         | 459   | 74.8        | 110    | 2 S44110 | Ig heavy chain V-D |
| 24         | 458   | 74.6        | 139    | 2 A41287 | Ig heavy chain pre |
| 25         | 457   | 74.4        | 118    | 2 A26340 | Ig heavy chain pre |
| 26         | 454   | 73.9        | 97     | 2 PLO118 | Ig heavy chain V-I |
| 27         | 454   | 73.9        | 97     | 2 S26899 | Ig heavy chain V r |
| 28         | 452   | 73.6        | 135    | 2 S31604 | Ig heavy chain V r |
| 29         | 451   | 73.5        | 118    | 2 S20780 | Ig heavy chain V r |

|    |       |      |     |          |                    |
|----|-------|------|-----|----------|--------------------|
| 30 | 451   | 73.5 | 129 | 2 S44114 | Ig heavy chain V r |
| 31 | 448   | 73.0 | 99  | 2 S12418 | Ig heavy chain V r |
| 32 | 447.5 | 72.9 | 139 | 2 S31696 | Ig heavy chain V r |
| 33 | 445.5 | 72.6 | 137 | 2 S31585 | Ig heavy chain V r |
| 34 | 445.5 | 72.6 | 140 | 2 A49045 | Ig heavy chain V r |
| 35 | 445   | 72.5 | 120 | 2 PT0370 | Ig mu chain precu  |
| 36 | 444   | 72.3 | 126 | 2 S47010 | Ig heavy chain V4. |
| 37 | 443   | 72.1 | 99  | 2 S26800 | Ig heavy chain V r |
| 38 | 442   | 72.0 | 99  | 2 S12412 | Ig heavy chain V r |
| 39 | 442   | 72.0 | 105 | 2 S44125 | Ig lambda chain V  |
| 40 | 442   | 72.0 | 118 | 2 S24443 | Ig heavy chain V r |
| 41 | 442   | 72.0 | 140 | 2 S78052 | Ig heavy chain pre |
| 42 | 441.5 | 71.9 | 98  | 2 S12421 | Ig heavy chain V r |
| 43 | 441.5 | 71.9 | 132 | 2 A38911 | Ig heavy chain V r |
| 44 | 441.5 | 71.9 | 140 | 2 A24770 | hypothetical hybr  |
| 45 | 441   | 71.8 | 97  | 2 S26906 | Ig heavy chain V r |

## ALIGNMENTS

## RESULT 1

S78051 Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)

C:Species: Homo sapiens (man)

C&gt;Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999

C/Accession: S78051; S23716

R:Harindranath, N.  
submitted to the EMBL Data Library, August 1990

A:Reference number: S78051

A:Accession: S78051

A:Molecule type: mRNA

A:Residues: 1-135 &lt;HAR&gt;

A:Cross-references: EMBL:X5437; NID:937814; PIDN:CA48306.1; PID:9530117

R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockins

Int. Immunol. 3, 865-875, 1991

A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and hu

patient.  
A:Reference number: S23716; MUID:92031262; PMID:1178404

A:Accession: S23716

A:Molecule type: mRNA

A:Residues: 13-111 &lt;HAW&gt;

A:Cross-references: EMBL:X5437

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:1-13/Domain: signal sequence (fragment) #status predicted &lt;SIG&gt;

F:14-135/Product: Ig heavy chain (fragment) #status predicted &lt;MAT&gt;

F:27-111/Domain: immunoglobulin homology &lt;IMW&gt;

Query Match 81.7%; Score 501.5; DB 2; Length 135;  
Best Local Similarity 82.2%; Pred. No. 2.4e-38;  
Matches 97; Conservative 6; Mismatches 10; Indels 5; Gaps 2;

QY 2 EBSGGLVKSQTLSTCTVSGSIRSGYWSWIRPGKLEWIGYVHSGNTYVPSL 61  
DB 18 EBSGGLVKSQTLSTCTVSGSIRSGYWSWIRPGKLEWIGYVHSGNTYVPSL 77  
QY 62 KSRVTMSVDSIKNPSLRISVTAADTAIVVYCAR--SDGYTLDN--WGQGLTVTVSS 114  
DB 78 KSRVTISVDSIKNPSLRISVTAADTAIVVYCARLGPDDYTLDMQMDVWGQGLTVTVSS 135

## RESULT 2

S13519 Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C&gt;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S13519

R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked

A:Reference number: S13519; MUID:91187691; PMID:2011536

A:Accession: S13519

A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-147 <MAR>  
 A:Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:41-125/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 497.5; DB 2; Length 147;  
 Best Local Similarity 82.8%; Pred. No. 66-38;  
 Matches 96; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 61  
 DB 32 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 91

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDG---DGYTLDMNGGTLVTYSS 114  
 DB 92 KSRVTISVDTSKNQFSLKLSSTVADTAAYVYCARPLLMGELFDYWGQGLTVTVSS 147

### RESULT 3

I37782  
 Ig variable region (VDJ) (clone T23-9) - human (fragment)

C:Species: Homo sapiens (man)  
 C>Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
 C:Accession: J37782; S25476  
 R:Demaison, C.; Chateigner, P.; Theze, J.; Zouali, M.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
 A>Title: Somatic diversification in the heavy chain variable region genes expressed by B  
 A:Reference number: A36876; MID:94119917; PMID:8290556  
 A:Accession: J37782  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-140 <RES>  
 A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 492.5; DB 2; Length 140;  
 Best Local Similarity 82.2%; Pred. No. 1.6e-37;  
 Matches 97; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 61  
 DB 25 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 82

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDG---GYTLDMNGGTLVTYSS 114  
 DB 83 KSRVTISVDTSKNQFSLKLSSTVADTAAYVYCARHNSSSWYGRYFDYWGQGLTVTVSS 140

### RESULT 4

S30534  
 Ig heavy chain V region - human

C:Species: Homo sapiens (man)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
 C:Accession: S30534  
 R:Marlette, X.  
 submitted to the EMBL Data Library, October 1992  
 A:Reference number: S30520  
 A:Accession: S30534  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-130 <MAR>  
 A:Cross-references: EMBL:Z18320  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 490; DB 2; Length 130;  
 Best Local Similarity 78.4%; Pred. No. 2.5e-37;  
 Matches 98; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 61  
 DB 11 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 68

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 61

DB 6 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDG---GYTLDMNGGTLVTYSS 109  
 DB 66 KSRVTISVDTSKNQFSLKLSSTVADTAAYVYCARPLLMGELFDYWGQGLTVTVSS 125

QY 110 VTYSS 114  
 DB 126 VTYSS 130

### RESULT 5

S37456  
 Ig mu chain - human (fragment)

C:Species: Homo sapiens (man)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
 C:Accession: S37456  
 R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
 submitted to the EMBL Data Library, September 1993  
 A:Description: Cloning and analysis of human Igm anti-Thyroglobulin autoantibodies from  
 A:Reference number: S37453  
 A:Accession: S37456  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-116 <MC1>  
 A:Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:6-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 488.5; DB 2; Length 116;  
 Best Local Similarity 81.2%; Pred. No. 3e-37;  
 Matches 95; Conservative 7; Mismatches 6; Indels 9; Gaps 2;

QY 6 GLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 65  
 DB 1 GLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 60

QY 66 TMSVDTSKNHFSLRLSSVTADTAAYVYCARSDG---LDNMNGGTLVTYSS 114  
 DB 61 TISVDTSKNQFSLKLSSTVADTAAYVYCARG-GYGYGYYYVDMWGKGLTVTVSS 116

### RESULT 6

S31690  
 Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S31690  
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
 submitted to the EMBL Data Library, June 1992  
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A:Reference number: S31585  
 A:Accession: S31690  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-130 <CU1>  
 A:Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:20-102/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 487.5; DB 2; Length 130;  
 Best Local Similarity 78.7%; Pred. No. 4.2e-37;  
 Matches 96; Conservative 5; Mismatches 10; Indels 11; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 61  
 DB 11 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYYPSTL 68

|    |     |  |                |     |
|----|-----|--|----------------|-----|
| Oy | 62  | KSRVTMSVPTSKNHFLRLSSVTAADTAVYYCARSDG-----                  | -TLIDWGCGGLLVY | 112 |
|    | :   | :  | :              | :   |
|    | :   | :  | :              | :   |
|    | :   | :  | :              | :   |
|    | :   | :  | :              | :   |
|    | :   | :  | :              | :   |
| Dd | 69  | KSRVTTISVDTSKKNQFSLKLSTVAADTAVYYCARSSVLIMFGELLYFDYIWGGLLVY |                | 128 |
|    | :   | :  | :              | :   |
|    | :   | :  | :              | :   |
| Oy | 113 | SS 114   |                |     |
|    | :   | :  |                |     |
| Dd | 129 | SS 130   |                |     |

## RESULT 7

Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C/Accession: S44113  
R/Hawkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r  
A/Reference number: S44105  
A/Accession: S44113  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-121 <HAW>  
A/Cross-references: EMBL:Z31389, NID:G472967, PIDN:CNA63264.1; PID:G940524  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-95/Domain: immunoglobulin homology <IIM>

|                       |                 |                    |           |             |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match           | 78.3%           | Score 480.5;       | DB 2;     | Length 121; |
| Best Local Similarity | 80.2%;          | Pred. No. 1.7e-36; |           |             |
| Matches 93;           | Conservative 6; | Mismatches 14;     | Indels 3; | Gaps 2      |

QY 2 ESGPGLVKPSQTLSTCTVYGGGSRGGYYWMSAIRQPPGKGLEWGIYIYHSGNTYINPSL 61

DB 6 ESGPGLVKPSELTSLCTVYGGGYSISSSYWGMTRQPPGKGLEWGISIYYSGSTYINPSL 65

```

QY      62 KSRVTMSVDTSKXHFSLRLSSVTADTAIVYCAR-SDGY--TLDNMGCGTLVTVSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      66 KSRVLTISVDTSKNQFSLKLTSSVTADTGVYCSRLSGGYSDPFDYWSQGLTVTVSS 121

```

## RESULT 8

Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: G31511  
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A:Reference number: G31509  
A:Accession: G31511  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69866; NID:G33094; PIDN:CAA49500.1; PID:G33095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
E:47-129/Domain: immunoglobulin homology <IMM>

|                       |        |                    |       |                |
|-----------------------|--------|--------------------|-------|----------------|
| Query March           | 78.1%; | Score 479.5;       | DB 2; | Length 155;    |
| Best Local Similarity | 77.5%; | Pred. No. 2.7e-36; |       |                |
| Matches               | 93;    | Conservative       | 8;    | Mismatches 10; |
|                       |        |                    |       | Indels 9;      |
|                       |        |                    |       | Gaps 2         |

```

QY      2  ESGPGLVKPSQTLSTCTVSGGSIRSGGIYWSMIQPPGKLEWICGIYHSNCTYTNPSL 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB     38  ESGPGLVKPSQTLSTCTVSGGSIRSGGIYWSMIQPPGKLEWICGIYHSNCTYTNPSL 95

```

```
QY      62 KSRVTMSVDTSKNHFSRLSSVTAADPAVYVCARSDG-----YTLDNWGCGTLVYSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      96 KSRVTISVDTSKNQFSLKSVSTAAADPAVYVCARGGGSSWYDYGYGMDVWGCGTIVYSS 155
```

## RESULT 9

Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S09710  
 R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of  
A:Reference number: S09710; MUID:90262535; PMID:211699

A;Residues:1-146 <HUG>  
A;Cst08- references: GB:X52110, NID:g31447, PID:CAA36344.1, PID:g31448  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;34-118/Domain: immunoglobulin homology <IMW>

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 77.8%;           | Score 477.5;       | DB 2;      | Length 146; |
| Best Local Similarity | 74.0%;           | Pred. No. 3.8e-36; |            |             |
| Matches 91;           | Conservative 11; | Mismatches 10;     | Indels 11; | Gaps 2;     |

```

QY      2  ESGPGLVKPSQTLSTLCVSGSIRSGGYMSWIRQPKGLGIEWGYIYHSGNTYNPSTL 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      25  ESGPGLVKPSETLSTLCVSGSGSVSSGGLYMGWVRQPKGLGIEWGISIFYSGSTYNPSTL 84

```

```

QY      62 KSRVTMSVDTSKNHSLSRLSSVTAADTAVVYCARSDGY-----TLDMNGGGTIVT 111
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      85 KSRVTIISVDTLKNNFSLSKSSVTAADTAVVYCTR-PEYGDITSVRKRYVMNDLWGQGTIVT 143

```

|    |     |     |     |
|----|-----|-----|-----|
| QY | 112 | VSS | 114 |
|    |     |     |     |
| Db | 144 | VSS | 146 |

RESULT 10

Ig heavy chain human  
 C.Species: Homo sapiens (man)  
 C.Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1995  
 C.Accession: S31512  
 R.Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
 submitted to the EMBL Data Library, December 1992  
 A.Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
 A.Reference number: S31509  
 A.Accession: S31512  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-155 <CHA>  
 A.Cross-references: EMBL:X69860; NID:G33082; PIDN:CAA9494.1; PID:G33083  
 C.Superfamily: immunoglobulin V region; immunoglobulin homology  
 C.Keywords: heterotetramer; immunoglobulin  
 F147-129/Domain: immunoglobulin homology <IMM>

|                          |       |                  |           |             |
|--------------------------|-------|------------------|-----------|-------------|
| Query Match              | 77.8% | Score 477.5;     | DB 2;     | length 155; |
| Best Local Similarity    | 76.7% | Pred. No. 4e-36; |           |             |
| Matches 92; Conservative | 9;    | Mismatches 10;   | Indels 9; | Gaps 2;     |

```
QY      2  ESGPGLVKPSQTLSLTCTVSGSIRGGGYMSWIRQPGKGLEIGIYHSGMTYYNPSL 61
          |||||::||||| | | | | | | | | | | | | | | | | | | | | :
Db     38  ESGPGLVKPSSETLSLTCTVSGGSIS--YMSWIRQPGKGLEIGIYTYTGSATYNPPI 95
```

```

Qy      62 KSRVTMSVDTSKNHFSLRLSSVTAADTA VVYCARSDG-----YTLDNWGQGLVTVYSS 114
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      96 KSRVTISVDTSKNGSLKVVSVTAADTA VVYCARGGGISSWVYVYGGDVMWGQGITVTVYSS 154

```

## RESULT 11

Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C/Accession: S09711  
 R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coatswell, J.  
 Biochem. J. 268, 135-140, 1990  
 A>Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of  
 A/Reference number: S09710; M0ID:90262535; PMID:2111699  
 A/Accession: S09711  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1146 <HUG>  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotetramer; Immunoglobulin  
 F/34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 473.5; DB 2; Length 146;  
 Best Local Similarity 73.8%; Pred. No. 8.7e-36;  
 Matches 90; Conservative 10; Mismatches 13; Indels 9; Gaps 1;  
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPGKGLWIGIYHSGNTYYPNL 61  
 DB 25 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPGKGLWIGIYHSGNTYYPNL 84  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCAR-----SDGYLDNMGGTTLVTV 112  
 DB 85 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARVIVSRYSIQSYMDVMGKGTTLTV 144  
 QY 113 SS 114  
 DB 145 SS 146

## RESULT 12

S19668  
 Ig heavy chain V region (VH4DH6) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 20-Jun-2000  
 C/Accession: S19668; S24445  
 R/Marker, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
 A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph  
 A/Reference number: S19663; M0ID:92085276; PMID:1748994  
 A/Accession: S19668  
 A/Molecule type: mRNA  
 A/Residues: 1-127 <MAR>  
 A/Cross-references: EMBL:X61648  
 R:Jones, P.T.  
 Submitted to the EMBL Data Library, October 1991  
 A/Reference number: S24442  
 A/Accession: S24445  
 A/Molecule type: mRNA  
 A/Residues: 1-118 'E', 120-121 'T', 123-126 'F' <JON>  
 A/Cross-references: EMBL:X61648; NID:937722; PIDN:CAA3829.1; PID:91335380  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;  
 Best Local Similarity 74.6%; Pred. No. 9.2e-36;  
 Matches 91; Conservative 9; Mismatches 13; Indels 9; Gaps 1;  
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPGKGLWIGIYHSGNTYYPNL 61  
 DB 6 QSGSGLVKPSQTLSTCTVSGSIRSGGYWMIROPGKGLWIGIYHSGNTYYPNL 65  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARSDG-----YTLDNMGGTLTVTV 112  
 DB 66 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARSDG-----YTLDNMGGTLTVTV 125  
 QY 113 SS 114  
 DB 126 SS 127

## RESULT 13

S31514  
 Ig heavy chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
 C/Accession: S31514  
 R:Chastagner, P.; Demaison, C.; These, J.; Zouali, M.  
 submitted to the EMBL Data Library, December 1992  
 A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
 A/Reference number: S31509  
 A/Accession: S31514  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-128 <CHA>  
 A/Cross-references: EMBL:X69862; NID:933086; PIDN:CAA9496.1; PID:933087  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotetramer; Immunoglobulin  
 F/22-106/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 128;  
 Best Local Similarity 78.4%; Pred. No. 9.3e-36;  
 Matches 91; Conservative 8; Mismatches 14; Indels 3; Gaps 1;  
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPGKGLWIGIYHSGNTYYPNL 61  
 DB 13 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPGKGLWIGIYHSGNTYYPNL 72  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCAR---SDGYLDNMGGTTLTVTV 114  
 DB 73 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARVIVSRYSIQSYMDVMGKGTTLTV 128

## RESULT 14

S31676  
 Ig heavy chain V region - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C/Accession: S31676  
 R:Guinier, A.M.; Gauchier, L.; Boulik, L.; Fougereau, M.; Tonnelie, C.  
 submitted to the EMBL Data Library, June 1992  
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A/Reference number: S31585  
 A/Accession: S31676  
 A/Molecule type: mRNA  
 A/Status: preliminary  
 A/Residues: 1-137 <CU>  
 A/Cross-references: EMBL:Z14182; NID:931031; PIDN:CAA76551.1; PID:931032  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 472; DB 2; Length 137;  
 Best Local Similarity 82.6%; Pred. No. 1.1e-35;  
 Matches 95; Conservative 4; Mismatches 12; Indels 4; Gaps 2;  
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPGKGLWIGIYHSGNTYYPNL 61  
 DB 25 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPGKGLWIGIYHSGNTYYPNL 82  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARSDG-----YTLDNMGGTLTVTV 114  
 DB 83 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARSDG-----YTLDNMGGTLTVTV 137

## RESULT 15

S26803  
 Ig heavy chain V region - human  
 C/Species: Homo sapiens (man)  
 C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 C/Accession: S26803  
 R/Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
 Eur. J. Immunol. 22, 1075-1082, 1992  
 A>Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.  
 A/Reference number: S26800; M0ID:92201299; PMID:1348029



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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 ; Search time 6.39091 Seconds  
(without alignments)  
838.855 Million cell updates/sec

Title: US-10-027-725A-9

Sequence: 1 LESGGLVPSQTLSTCTV.....RSDGTYLDNMGGTLYTVSS 114  
614

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 439.5 | 71.6        | 129    | 1  | HV2F_HUMAN  |
| 2          | 420   | 68.4        | 146    | 1  | HV2I_HUMAN  |
| 3          | 393.5 | 64.1        | 117    | 1  | HV2G_HUMAN  |
| 4          | 372.5 | 60.7        | 137    | 1  | HV46_MOUSE  |
| 5          | 357.5 | 58.2        | 113    | 1  | HV47_MOUSE  |
| 6          | 349.5 | 56.9        | 144    | 1  | HV43_MOUSE  |
| 7          | 348.5 | 56.8        | 116    | 1  | HV61_MOUSE  |
| 8          | 347   | 56.5        | 117    | 1  | HV62_MOUSE  |
| 9          | 342.5 | 55.8        | 116    | 1  | HV60_MOUSE  |
| 10         | 330   | 53.7        | 135    | 1  | HV02_XENLA  |
| 11         | 313   | 51.0        | 120    | 1  | HV2B_HUMAN  |
| 12         | 302.5 | 49.3        | 119    | 1  | HV2C_HUMAN  |
| 13         | 293.5 | 47.8        | 136    | 1  | HV01_XENLA  |
| 14         | 291   | 47.4        | 122    | 1  | HV3A_HUMAN  |
| 15         | 289.5 | 47.1        | 125    | 1  | HV2D_HUMAN  |
| 16         | 289   | 47.1        | 114    | 1  | HV3B_HUMAN  |
| 17         | 288   | 46.9        | 115    | 1  | HV44_MOUSE  |
| 18         | 288   | 46.9        | 147    | 1  | HV2H_HUMAN  |
| 19         | 287.5 | 46.8        | 121    | 1  | HV2E_HUMAN  |
| 20         | 287   | 46.7        | 119    | 1  | HV40_MOUSE  |
| 21         | 286.5 | 46.7        | 117    | 1  | HV2B_RABIT  |
| 22         | 282   | 45.9        | 122    | 1  | HV3G_HUMAN  |
| 23         | 280   | 45.6        | 126    | 1  | HV2A_HUMAN  |
| 24         | 278   | 45.3        | 116    | 1  | HV05_CARAU  |
| 25         | 277.5 | 45.2        | 121    | 1  | HV3J_HUMAN  |
| 26         | 277   | 45.1        | 119    | 1  | HV3J_HUMAN  |
| 27         | 276   | 45.0        | 116    | 1  | HV45_MOUSE  |
| 28         | 276   | 45.0        | 116    | 1  | HV2C_RABIT  |
| 29         | 275   | 44.8        | 139    | 1  | HV2C_RABIT  |
| 30         | 274   | 44.6        | 114    | 1  | HV2A_RABIT  |
| 31         | 272.5 | 44.4        | 117    | 1  | HV41_MOUSE  |
| 32         | 272.5 | 44.4        | 117    | 1  | HV42_MOUSE  |
| 33         | 272   | 44.3        | 122    | 1  | HV3H_HUMAN  |

|    |       |      |     |   |            |             |
|----|-------|------|-----|---|------------|-------------|
| 34 | 271.5 | 44.2 | 142 | 1 | HV01_RAT   | P01805 ratu |
| 35 | 268   | 43.6 | 139 | 1 | HV07_MOUSE | P01751 mus  |
| 36 | 263.5 | 42.9 | 115 | 1 | HV3D_HUMAN | P01765 mus  |
| 37 | 263   | 42.8 | 118 | 1 | HV51_MOUSE | P06330 mus  |
| 38 | 263   | 42.8 | 122 | 1 | HV20_MOUSE | P01789 mus  |
| 39 | 262.5 | 42.8 | 117 | 1 | HV12_MOUSE | P01756 mus  |
| 40 | 262   | 42.7 | 120 | 1 | HV50_MOUSE | P06329 mus  |
| 41 | 262   | 42.7 | 126 | 1 | HV3K_HUMAN | P01772 homo |
| 42 | 262   | 42.7 | 136 | 1 | HV16_MOUSE | P01783 mus  |
| 43 | 261.5 | 42.6 | 115 | 1 | HV3F_HUMAN | P01767 homo |
| 44 | 261.5 | 42.6 | 117 | 1 | HV13_MOUSE | P01757 mus  |
| 45 | 258.5 | 42.1 | 117 | 1 | HV17_MOUSE | P01786 mus  |

## ALIGNMENTS

## RESULT 1

| ID | HV2F_HUMAN  | STANDARD | PRT | 129 AA |
|----|---|----------|-----|--------|
| AC | P01824  |          |     |        |
| DT | 21-JUL-1986 (Rel. 01, Created)                                    |          |     |        |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update)                       |          |     |        |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update)                     |          |     |        |
| DE | Ig heavy chain V-II region WAI.                                   |          |     |        |
| OS | Homo sapiens (Human).   |          |     |        |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |          |     |        |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.         |          |     |        |
| OX | NCB1_TaxID=9606;  |          |     |        |
| RN | [1]   |          |     |        |
| RP | SEQUENCE.   |          |     |        |
| RA | MEDLINE=8222235; PubMed=680618;                                   |          |     |        |
| RA | Takanaishi N., Teraert D., Debure B., Lin L.-C., Putnam F.W.;     |          |     |        |
| RT | "Complete amino acid sequence of the delta heavy chain of human   |          |     |        |
| RT | immunoglobulin D.";   |          |     |        |
| RL | Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).                 |          |     |        |
| CC | -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA    |          |     |        |
| CC | PROTEIN.  |          |     |        |
| CC | -I- SIMILARITY: Contains 1 immunoglobulin-like domain.            |          |     |        |
| DR | PIR, A02099; D2HUMA.  |          |     |        |
| DR | HSSP; P01825; 7FAB.   |          |     |        |
| DR | GlycoSuiteDB; P01824; -.  |          |     |        |
| DR | GO; GO:0005576; C:extracellular; NAS.                             |          |     |        |
| DR | GO; GO:0003823; F:antigen binding activity; NAS.                  |          |     |        |
| DR | GO; GO:0006955; P:immune response; NAS.                           |          |     |        |
| DR | InterPro; IPR007110; Ig-like.                                     |          |     |        |
| DR | InterPro; IPR003006; Ig-MHC.                                      |          |     |        |
| DR | InterPro; IPR003596; Ig_V.  |          |     |        |
| DR | Pfam; PF00047; Ig_1.  |          |     |        |
| DR | SMART; SM00406; IGV_1.  |          |     |        |
| DR | PROSITE; PS50835; IG_LIKE; 1.                                     |          |     |        |
| KW | Immunoglobulin V region.  |          |     |        |
| FT | DOMAIN 1 113 IG-LIKE.   |          |     |        |
| FT | NON TER 129 129   |          |     |        |
| SQ | SEQUENCE 129 AA; 14117 MW; DSD53D47ABE51319 CRC64;                |          |     |        |

Query Match 71.6%; Score 439.5; DB 1; Length 129;  
Best Local Similarity 66.7%; Pred. No. 4.2e-39;  
Matches 84; Conservative 12; Mismatches 15; Indels 15; Gaps 2;

|    |     |   |     |
|----|-----|---|-----|
| QY | 2   | ESGGLVPSQTLSTCTVSGGSTRSGGYMSWIRPQKGLWIGVYHSGNRYNPSL | 61  |
| DB | 6   | ESGGLVPSQTLSTCTVSGGSTRSGGYMSWIRPQKGLWIGVYHSGNRYNPSL | 65  |
| QY | 62  | KSRVTSVDTSKNPSLRLSSVTADPAVYVCAR-----SDGTYLDNMGGT    | 108 |
| DB | 66  | KSRVTSVDTSKNPSLRLSSVTADPAVYVCAR-----SDGTYLDNMGGT    | 123 |
| QY | 109 | LTVVSS 114  |     |
| DB | 124 | TWVSS 129   |     |

```
RESULT 2
HV21_HUMAN          STANDARD;          PRT;          146 AA.
ID   HV21_HUMAN
AC   P06331
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-II region ARH-77 precursor.
OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxId=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85205332; PubMed=3922855;
RA   Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT   "A cloned human immunoglobulin heavy chain gene with a novel direct-
RL   Gene 33:181-189 (1985).
PIR   A02101; G1H02.
DR   HSSP; P01825; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IgV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1          19
FT   CHAIN           20         146
FT   DOMAIN          20         117
FT   DOMAIN          118        127
FT   DOMAIN          128        146
FT   DISULFID        42         115
FT   NON_TER         146        146
SQ   SEQUENCE        146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match          68.4%; Score 420; DB 1; Length 146;
Best Local Similarity 71.1%; Pred. No. 5.3e-37;
Matches 86; Conservative 7; Mismatches 16; Indels 12; Gaps 3;

QY   4 GPGLVKPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGYIHSGNTYNSLKS 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB   28 GAGLVKPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGYIHSGNTYNSLKS 85
QY   64 RVTMSVDTSKNHFSLRLSVTAADTAIVYYCARSDG-----YTLDMNGQGLVTVSS 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB   86 RVTISLDTSKNLFSLRLSVTAADTAIVYYCARGLGNGMNDVYYGMDVWGQGTIVTVSS 145
QY   114 S 114
DB   146 S 146

RESULT 3
HV2G_HUMAN          STANDARD;          PRT;          117 AA.
ID   HV2G_HUMAN
AC   P01825;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region MEMM.
OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxId=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77242302; PubMed=407927;
RA   Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
```

```
RT   "Amino acid sequence of the VH region of a human myeloma
RL   immunoglobulin (IGG New).";
RL   Biochemistry 16:3412-3420 (1977).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RX   MEDLINE=78066916; PubMed=618887;
RA   Saul F.A., Amel L.M., Poljak R.J.;
RT   "Preliminary refinement and structural analysis of the Fab fragment
RT   from human immunoglobulin new at 2.0-A resolution.";
RL   J. Biol. Chem. 253:585-597 (1978).
CC   -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC   PROTEIN.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A90404; G1HUM.
DR   PDB; 7FAB; 31-JAN-94.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IgV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3d-structure; Pyrrolidone carboxylic acid.
FT   DOMAIN          1          111
FT   MOD_RES         1          1
FT   STRAND          3          7
FT   STRAND          11         12
FT   TURN            14         15
FT   TURN            18         25
FT   TURN            30         31
FT   TURN            33         39
FT   TURN            41         42
FT   STRAND          46         51
FT   TURN            53         54
FT   STRAND          57         59
FT   HELIX           61         63
FT   TURN            64         66
FT   STRAND          67         72
FT   TURN            73         76
FT   STRAND          77         82
FT   STRAND          87         89
FT   HELIX           91         98
FT   STRAND          104        107
FT   STRAND          111        115
FT   NON_TER         117        117
SQ   SEQUENCE        117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match          64.1%; Score 393.5; DB 1; Length 117;
Best Local Similarity 67.5%; Pred. No. 2.4e-34;
Matches 77; Conservative 16; Mismatches 18; Indels 3; Gaps 2;

QY   2 ESGPGLVKSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGYIHSGNTYNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB   6 QSGPGLVKSQTLSTCTVSGSGTFSND--YYTWVROPKGLGEMIGYFHHGTSDDTTPPL 63
QY   62 KSRVTMSVDTSKNHFSLRLSVTAADTAIVYYCARSDG-----YTLDMNGQGLVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB   64 RSRVTMLVDTSKNHFSLRLSVTAADTAIVYYCARNLIGCIDVWGQGSIVTVSS 117

RESULT 4
HV46_MOUSE          STANDARD;          PRT;          137 AA.
ID   HV46_MOUSE
AC   P01822;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig heavy chain V region MOPC 315 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxId=10116;
```



NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A. PubMed=2497341;  
 MEDLINE=89238351;  
 RA Riffert A., Horne C., Dorrington K.J., Klein M.;  
 "Cloning, sequencing and expression of the rearranged MOPC 315 VH  
 gene segment";  
 RL Mol. Immunol. 26:431-434 (1989).  
 [2]  
 SEQUENCE OF 1-31.  
 RX MEDLINE=78094475; PubMed=414225;  
 RA Jilka R.L., Pestka S.;  
 "Amino acid sequence of the precursor region of MOPC-315 mouse  
 immunoglobulin heavy chain";  
 RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).  
 [3]  
 SEQUENCE OF 1-21.  
 RX MEDLINE=79148758; PubMed=428562;  
 RA Schechter I., Wolf O., Zemel R., Burstein Y.;  
 "Structure and function of immunoglobulin genes and precursors";  
 RL Fed. Proc. 38:1839-1845 (1979).  
 [4]  
 SEQUENCE OF 19-136.  
 RX MEDLINE=74170779; PubMed=4524622;  
 RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;  
 "Amino acid sequence of the variable region of the heavy (alpha)  
 chain of a mouse myeloma protein with anti-hapten activity";  
 RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).  
 [5]  
 REVISION TO 53.  
 RX MEDLINE=77244979; PubMed=268248;  
 RA Hood L., Margolies M.N., Givol D., Zakut R.;  
 Unpublished results, cited by:  
 RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;  
 Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).  
 CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA  
 PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.  
 -----  
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 -----  
 CC EMBL; M27638; AAA61337.1; -;  
 DR EMBL; X07880; CA30727.1; -;  
 DR PIR; P0102; AVMS35.  
 DR HSSP; P01825; 7FAB.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.  
 FT DOMAIN 19 48 FRAMEWORK-1.  
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 85 116 FRAMEWORK-3.  
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 127 137 FRAMEWORK-4.  
 FT DISULFID 40 114 BY SIMILARITY.  
 FT CONFLICT 15 15 G-> GG (IN REF. 1; CAA30727).  
 FT CONFLICT 15 15 G-> H (IN REF. 2).  
 FT CONFLICT 77 78 GY-> YG (IN REF. 4).  
 FT CONFLICT 102 102 N-> D (IN REF. 4).  
 FT CONFLICT 123 123 MISSING (IN REF. 4).  
 FT NON\_TER 137 137

SEQ SEQUENCE 137 AA; 1539 MW; FB3828304C2B81DC CRC64;  
 Query Match 60.7%; Score 372.5; DB 1; Length 137;  
 Best Local Similarity 62.6%; Pred. No. 4.6e-32;  
 Matches 71; Conservative 16; Mismatches 22; Indels 3; Gaps 2;  
 QY 2 ESGPGLVPSQTLILCTVSGSGSIRSGGYWSWTRPGKLEWIGYIYHSGNTYNSPL 61  
 DB 24 ESGPGLVPSQSLSTLSVSGYSITS-GYFMNWRQFPGKLEWIGIKYDGSNGYNSPL 82  
 QY 62 KSRVTMSVDTSKNHFSLRSSVTADTAIVYCARSDG-YTLDNWGCGTLVTVSS 114  
 DB 83 KNRVTSIRDTSENQFELKINSVTTEDTATYTCAGDNDHLYFDYWGCGTLVTVSS 137  
 RESULT 5  
 ID HV47 MOUSE STANDARD; PRT; 113 AA.  
 AC P01823;  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 36-60.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=84024551; PubMed=6414509;  
 RA Juzczak E.C., Margolies M.N.;  
 "Amino acid sequence of the heavy chain variable region from the A/J  
 mouse anti-arsenate monoclonal antibody 36-60 bearing a minor  
 idiotype";  
 RL Biochemistry 22:4291-4296 (1983).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTARSONATE  
 MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND  
 IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTARSONATE RESPONSE OF  
 STRAIN A/J MICE.  
 CC CC  
 CC PIR; A02098; G2MS60.  
 DR PDB; 1J10; 18-FEB-03.  
 DR PDB; 1J1P; 18-FEB-03.  
 DR PDB; 1J1X; 18-FEB-03.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; 3D-structure.  
 FT NON\_TER 113 113  
 FT SEQUENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;  
 Query Match 58.2%; Score 357.5; DB 1; Length 113;  
 Best Local Similarity 62.8%; Pred. No. 1.4e-30;  
 Matches 71; Conservative 16; Mismatches 21; Indels 5; Gaps 2;  
 QY 2 ESGPGLVPSQTLILCTVSGSGSIRSGGYWSWTRPGKLEWIGYIYHSGNTYNSPL 61  
 DB 6 ESGPGLVPSQTLILCTVSGSITSD--YNNWRKRPQNLKLEHMGYSISGSGTYNSPL 63  
 QY 62 KSRVTMSVDTSKNHFSLRSSVTADTAIVYCARSDGTYTLDNWGCGTLVTVSS 114  
 DB 64 KSRISITRDTSKNQYLIQNLNSVTSBDAITYCT---SLRFAYWGCGTLVTVSA 113  
 RESULT 6  
 ID HV43 MOUSE STANDARD; PRT; 144 AA.  
 AC P01819;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Mus heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; V00768; CAA24149.1; -.
DR PIR; A02094; G2MS14.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT DOMAIN 20 130 IG-LIKE.
FT NON_TER 144 144
FT FT 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 56.9%; Score 349.5; DB 1; Length 144;
Best Local Similarity 59.0%; Pred. No. 1.2e-29;
Matches 72; Conservative 18; Mismatches 21; Indels 11; Gaps 3.

QY 2 ESGPGLVPSQTLSLTCTVSGGSIKSGGYVSWIRPGPKGLWIGYLYHSGNTYVNSL 61
DB 25 ESGPGLVAPSGSLSLTCTVSGGSL--GYGVVWVWQPPGKGLWIGYLYHSGNTYVNSL 82
QY 62 KSRVTMSVDTSKHHFSLRLSLSYTAADTVAYYCA-----RSDGY-TLDNWGGTILTV 112
DB 83 KSRLLTITKDNSSKSGVFLKMNLSLOTDDTARYYCAVSIIYYGSDRYFTLDYWGQGTSTLV 142
QY 113 SS 114
DB 143 SS 144

RESULT 7
HVL_MOUSE STANDARD; PRT; 116 AA.
ID HVL_MOUSE
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 1B43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;

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|                       |   |
|-----------------------|---|
| RX                    | MEDLINE=89279149; PubMed=249654;  |
| RA                    | Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  |
| RT                    | "Early onset of somatic mutation in immunoglobulin VH genes during<br>the primary immune response." |
| RL                    | J. Exp. Med. 169:2007-2019(1989).   |
| CC                    | -I JSCHELAEBOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.                                     |
| DR                    | PIR: J050508; HVMS1B.   |
| DR                    | PDB: 1KCS; 11-MAY-02.   |
| DR                    | IInterPro: IPR007110; IG-like.  |
| DR                    | IInterPro: IPR003006; IG_MHC.   |
| DR                    | IInterPro: IPR003596; IG_V.   |
| DR                    | pfam: PF00047; Ig; 1.   |
| DR                    | SMART: SM00406; IGV; 1.   |
| DR                    | PROSITE: PS50835; IG LIKE; 1.   |
| KW                    | Immunoglobulin V region; Signal; 3d-structure.  |
| FT                    | SIGNAL  |
| FT                    | CHAIN   |
| FT                    | DOMAIN  |
| FT                    | DOMAIN  |
| FT                    | DOMAIN  |
| FT                    | DOMAIN  |
| FT                    | DISULFID  |
| FT                    | NON TER   |
| SEQ                   | SEQUENCE  |
| Query Match           | 56.8%; Score 348.5; DB 1; Length 116;   |
| Best Local Similarity | 71.3%; Pred. No. 1.2e-29;   |
| Matches               | 67; Conservative 11; Mismatches 15; Indels 1; Gaps 1.   |
| Oy                    | 2 ESGGGLVKEQSTSLTCTVGSGSIRSGGYWSWIRPGPKGLEWGIYHSGNTYYNSL 61   |
| Dd                    | 24 ESGDPLVPSOSLSLTCTVTYSITS-GYSNHWIRQFPGNKLBNWGIIYHSNTSYNSPL 82                                     |
| Oy                    | 62 KSRVTMSVDTSKNHFSLRSSVTADPZAVVYCARG 95  |
| Dd                    | 83 KSRSITRDTSKNOEFLQNLNVTTEDATYYCAR 116   |
| RESULT 8              |   |
| HV62_MOUSE            | STANDARD; PRT; 117 AA.  |
| ID _HV62_MOUSE        |   |
| AC                    | P16533.   |
| DT                    | 01-NOV-1990 (Rel. 16, Created)  |
| DT                    | 01-NOV-1990 (Rel. 16, Last sequence update)   |
| DE                    | 15-SEP-2003 (Rel. 42, Last annotation update)   |
| DE                    | IG heavy chain V region 733 precursor.  |
| OS                    | Mus musculus (Mouse).   |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                                   |
| OC                    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.                                  |
| OX                    | NCB1_TaxID=10090;   |
| RN                    | [1]   |
| RP                    | SEQUENCE FROM N.A.  |
| RC                    | STRAIN=BALB/CJ;   |
| RX                    | MEDLINE=89279149; PubMed=249654;  |
| RA                    | Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  |
| RT                    | "Early onset of somatic mutation in immunoglobulin VH genes during<br>the primary immune response." |
| RL                    | J. Exp. Med. 169:2007-2019(1989).   |
| CC                    | -I SIMILARITY: Contains 1 immunoglobulin-like domain.   |
| DR                    | PIR: J050510; HVMS73.   |
| DR                    | HSSP: P01825; 7EAB.   |
| DR                    | IInterPro: IPR007110; IG-like.  |
| DR                    | IInterPro: IPR003006; IG_MHC.   |
| DR                    | IInterPro: IPR003596; IG_V.   |
| DR                    | pfam: PF00047; Ig; 1.   |
| DR                    | SMART: SM00406; IGV; 1.   |
| DR                    | PROSITE: PS50835; IG LIKE; 1.   |
| KW                    | Immunoglobulin V region; Signal.  |
| FT                    | SIGNAL  |
| FT                    | CHAIN   |
| FT                    | DOMAIN  |
| FT                    | DOMAIN  |
| FT                    | DOMAIN  |
| FT                    | DISULFID  |
| FT                    | NON TER   |
| SEQ                   | SEQUENCE  |
| Query Match           | 56.8%; Score 348.5; DB 1; Length 116;   |
| Best Local Similarity | 71.3%; Pred. No. 1.2e-29;   |
| Matches               | 67; Conservative 11; Mismatches 15; Indels 1; Gaps 1.   |
| Oy                    | 2 ESGGGLVKEQSTSLTCTVGSGSIRSGGYWSWIRPGPKGLEWGIYHSGNTYYNSL 61   |
| Dd                    | 24 ESGDPLVPSOSLSLTCTVTYSITS-GYSNHWIRQFPGNKLBNWGIIYHSNTSYNSPL 82                                     |
| Oy                    | 62 KSRVTMSVDTSKNHFSLRSSVTADPZAVVYCARG 95  |
| Dd                    | 83 KSRSITRDTSKNOEFLQNLNVTTEDATYYCAR 116   |

```

FT DISULFID 40 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517821F976BE CRC64;

Query Match
Best Local Similarity 56.5%; Score 347; DB 1; Length 117;
Matches 65; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKGLGEMIGYHSGNTYYNSL 61
DB 24 ESGPGLVPSQSLSTCTVSGTGYSLTS-YYHWMWIRQPGKGLGEMIGYHSGNTYYNSL 82
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR 95
DB 83 KKRISITRDTSKNPFLEKMSLTADTAIVYCAR 117

RESULT 9
HV60_MOUSE STANDARD; PRT; 116 AA.
ID HV60_MOUSE STANDARD; PRT; 116 AA.
AC P18531.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/CI;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR: J05059; HVMS31.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 18 IG HEAVY CHAIN V REGION M315.
FT SIGNAL 1 18
FT DOMAIN 19 116 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E5DC9E10 CRC64;

Query Match
Best Local Similarity 55.8%; Score 342.5; DB 1; Length 116;
Matches 64; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKGLGEMIGYHSGNTYYNSL 61
DB 24 ESGPGLVPSQSLSTCTVSGTGYSLTS-YYHWMWIRQPGKGLGEMIGYHSGNTYYNSL 82
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR 95
DB 83 KKRISITRDTSKNPFLEKMSLTADTAIVYCAR 116

RESULT 10
HV02_XENLA STANDARD; PRT; 135 AA.
ID HV02_XENLA STANDARD; PRT; 135 AA.

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AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains."
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC DR EMBL: J03632; AAA9791.1; -.
CC DR PIR: B31933; B31933.
CC DR HSSP: P01810; 2FBI.
CC DR InterPro: IPR007110; IG-1like.
CC DR InterPro: IPR003006; IG_MHC.
CC DR InterPro: IPR003596; IG_v.
CC DR Pfam: PF00047; Ig_1.
CC DR SMART: SM00406; IGV; 1.
CC DR PROSITE: PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
FT CHAIN 1 18 IG HEAVY CHAIN V REGION XIG14.
FT SIGNAL 1 18
FT DOMAIN 19 135 IG-1like.
FT CHAIN 20 128 IG-LIKE.
FT NON TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; BEC467105C00732E CRC64;

Query Match
Best Local Similarity 53.7%; Score 330; DB 1; Length 135;
Matches 65; Conservative 16; Mismatches 30; Indels 4; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKGLGEMIGYHSGNTYYNSL 61
DB 23 ESGGGLVPSQSLSTCTVSGFELSS-YYHWMWIRQPGKGLGEMIGYHSGNTYYNSL 80
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR--SDGYTLDMWGQTLTVSS 114
DB 81 KKRITITRDTSKNPFLEKMSLTADTAIVYCAR--SDGYTLDMWGQTLTVSS 135

RESULT 11
HV2B_HUMAN STANDARD; PRT; 120 AA.
ID HV2B_HUMAN STANDARD; PRT; 120 AA.
AC P01815.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region COR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;

```

RA Press E.M., Hogg N.M.;  
RT "The amino acid sequences of the Fd fragments of two human gamma-1  
heavy chains."  
RL Biochem. J. 117:641-660(1970).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
PROTEIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR: A02089; G1HUCO.  
DR HSSP: P01825; 7FAB.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 110  
FT MOD\_RES 1 110  
FT DISULFID 22 94  
FT CARBOHYD 62 62  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;  
Query Match 51.0%; Score 313; DB 1; Length 120;  
Best Local Similarity 56.3%; Pred. No. 6; 6e-26;  
Matches 67; Conservative 13; Mismatches 29; Indels 10; Gaps 3;  
QY 2 ESGPGVLRKPSQTLSTCTVSGSIRSGYWMIRPPCKGLEWIGYIHSGNTYNNPSL 61  
DB 6 ESGPVLVRPTQTLTCTFSGFSLSGTCVMGWMIRPPCKGLEWILAMDIDDKYNTSL 65  
QY 62 KSRVTSVDTSKNHSRLRSVTADTAAYVYCAR-----SDGYTLDMNGQGLVTVSS 114  
DB 66 ETRLTISKDTSRNVQLTMDPV---DTATYCARITVTPAPAY-MDVWGRGTPTVSS 120  
RESULT 12  
HV2C HUMAN STANDARD; PRT; 119 AA.  
AC P01816;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE 19 heavy chain V-II region DAM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=70258837; PubMed=5449120;  
RA Press E.M., Hogg N.M.;  
RT "The amino acid sequences of the Fd fragments of two human gamma-1  
heavy chains."  
RL Biochem. J. 117:641-660(1970).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE  
SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR: A02091; G1HUCO.  
DR HSSP: P01789; 1MCP.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Pyrrolidone carboxylic acid.

FT DOMAIN 1 113  
FT MOD\_RES 1 1  
FT NON\_TER 119 119  
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;  
Query Match 49.3%; Score 302.5; DB 1; Length 119;  
Best Local Similarity 53.5%; Pred. No. 8; 1e-25;  
Matches 61; Conservative 17; Mismatches 35; Indels 1; Gaps 1;  
QY 2 ESGPGVLRKPSQTLSTCTVSGSIRSGYWMIRPPCKGLEWIGYIHSGNTYNNPSL 61  
DB 6 ESGPVLVRPTQTLTCTFSGFSLSGTCVMGWMIRPPCKGLEWILAMDIDDKYNTSL 65  
QY 62 KSRVTSVDTSKNHSRLRSVTADTAAYVYCARSDG-YTLDMNGQGLVTVSS 114  
DB 66 ETRLVSKDTSRNVQLTMDPV---DTATYCARITVTPAPAY-MDVWGRGTPTVSS 119  
RESULT 13  
HV01 XENLA STANDARD; PRT; 136 AA.  
AC P20956;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE 19 heavy chain V region XIG8 precursor (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OC NCBI\_Taxid=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88176921; PubMed=2451244;  
RA Schwager J., Mikoyak C.A., Steiner L.A.;  
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced  
from cDNA sequence: implications for evolution of immunoglobulin  
domains."  
RT Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
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CC or send an email to [license@sib.ch](mailto:license@sib.ch)).  
CC -----  
DR EMBL: M20484; AAA49774.1; ALU\_TERM.  
DR PIR: A31933; A31933.  
DR HSSP: P01825; 7FAB.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Signal.  
FT SIGNAL 1 1  
FT CHAIN 19 18  
FT MOD\_RES 19 136  
FT NON\_TER 136 136  
SQ SEQUENCE 136 AA; 15123 MW; 3141839981441963 CRC64;  
Query Match 47.8%; Score 293.5; DB 1; Length 136;  
Best Local Similarity 52.1%; Pred. No. 8; 3e-24;  
Matches 61; Conservative 18; Mismatches 31; Indels 7; Gaps 3;  
QY 2 ESGPGVLRKPSQTLSTCTVSGSIRSGYWMIRPPCKGLEWIGYIHSGNTYNNPSL 61  
DB 23 ESGPGLVRSKPSRLRLCTVSGFSLTSGTCVMGWMIRPPCKGLEWILAMDIDDKYNTSL 80

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYC---ARSDGYTLDMNGGTLVTYSS 114  
 DB 81 KNRVTITKDNKGKQVYLOMNGEYKDYAMCYCTSTLGTAGY-FEHMGQGTMTVYTS 136

## RESULT 14

HV3A\_HUMAN STANDARD; PRT; 122 AA.

AC P01762;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region TRO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE (MYELOMA PROTEIN TRO).  
 RX MEDLINE=76023781; PubMed=809331;  
 RA Kratzin H., Altevogt P., Rudan E., Kortt A., Starosck K.,  
 RA Hilschmann N.;  
 RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),  
 RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III;  
 RT structure of the complete IgA-molecule." (1975).  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR: A02045; A1HUTR.  
 DR HSSP: P01772; 2P84.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG\_Like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.  
 FT DOMAIN 1 108 IG-LIKE.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 122 122  
 SQ SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

Query Match 47.4%; Score 291; DB 1; Length 122;  
 Best Local Similarity 47.5%; Pred. No. 1.3e-23;  
 Matches 57; Conservative 22; Mismatches 33; Indels 8; Gaps 3;

QY 1 EESGGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIYHSGNT-YYNP 59  
 DB 5 VQSGGGLVPGSGSLRLSCVAGSFPD--FYMSWIRZTRPGKGLZWVSYIGSGSGLYYAD 62  
 QY 60 SLKRVYMSVDTSKNHFSLRLSSVTADTAAYVYCARSDC-----YTLDMNGGTLVTYSS 114  
 DB 63 SVKGRFTISRDNQKSLYLZMBSLRTZBTAAYVYCAATBFBWSTSLBYWGGZBLVTYSS 122

## RESULT 15

HV2D\_HUMAN STANDARD; PRT; 125 AA.

AC P01817;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region MCE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=81118242; PubMed=6780622;  
 RA Geber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,  
 RA Litzman G.W.;  
 RT "Molecular basis for the temperature-dependent insolubility of  
 RT cryoglobulins. X. The amino acid sequence of the heavy chain variable  
 RT region of MCE.";  
 RL J. Immunol. 126:1212-1216(1981).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM  
 CC CRYOIMMUNOGLOBULIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR: A02092; MHHUMC.  
 DR HSSP: P01825; 7PAB.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG\_Like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.  
 FT DOMAIN 1 113 IG-LIKE.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 125 125  
 SQ SEQUENCE 125 AA; 13783 MW; 7A1ADP4C40F47BB5 CRC64;

Query Match 47.1%; Score 289.5; DB 1; Length 125;  
 Best Local Similarity 47.5%; Pred. No. 2e-23;  
 Matches 57; Conservative 20; Mismatches 36; Indels 7; Gaps 1;

QY 2 EESGGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIYHSGNTYYNP 61  
 DB 6 EESGGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIYHSGNTYYNP 65  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDCGT-----LDMNGGTLVTYSS 114  
 DB 66 RSRITGDTISRDNQVLTITMDPVDGTYCARPPRFTGNIGGFDXKMGCGTLVTYSS 125

Search completed: February 10, 2004, 18:36:30  
 Job time : 6.39091 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:24:13 ; Search time 26.9455 Seconds  
(without alignments)  
1091.761 Million cell updates/sec

Title: US-10-027-725A-9  
Perfect score: 614  
Sequence: 1 LESGRGLVPSQTLSTCTV.....RSDGYTLDMGQGLTVYSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioplasmid:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 470.5 | 76.6        | 119    | 4 Q9UL73  | Q9UL73 homo sapien  |
| 2          | 468   | 76.2        | 150    | 4 Q95973  | Q95973 homo sapien  |
| 3          | 460   | 74.9        | 496    | 4 Q96KX8  | Q96KX8 homo sapien  |
| 4          | 460   | 74.9        | 613    | 4 Q96CEX0 | Q96CEX0 homo sapien |
| 5          | 431   | 70.2        | 130    | 4 Q81ZD7  | Q81ZD7 homo sapien  |
| 6          | 429.5 | 70.0        | 588    | 4 Q8WUX4  | Q8WUX4 homo sapien  |
| 7          | 429.5 | 70.0        | 597    | 4 Q8WUX4  | Q8WUX4 homo sapien  |
| 8          | 429.5 | 70.0        | 618    | 4 Q96A66  | Q96A66 homo sapien  |
| 9          | 425.5 | 69.3        | 597    | 4 Q9A0B8  | Q9A0B8 homo sapien  |
| 10         | 412   | 67.1        | 473    | 4 Q8TC63  | Q8TC63 homo sapien  |
| 11         | 392.5 | 63.9        | 479    | 11 Q99M22 | Q99M22 mus musculu  |
| 12         | 364   | 59.3        | 122    | 4 Q9UL75  | Q9UL75 homo sapien  |
| 13         | 344.5 | 55.1        | 121    | 4 Q9UL96  | Q9UL96 homo sapien  |
| 14         | 340   | 55.4        | 121    | 11 Q99NG4 | Q99NG4 mus musculu  |
| 15         | 336   | 54.7        | 482    | 11 Q91X92 | Q91X92 mus musculu  |
| 16         | 314.5 | 51.2        | 118    | 4 Q9UL74  | Q9UL74 homo sapien  |

|    |       |      |     |           |                    |
|----|-------|------|-----|-----------|--------------------|
| 17 | 298.5 | 48.6 | 493 | 4 Q8NCL6  | Q8NCL6 homo sapien |
| 18 | 295   | 48.0 | 484 | 11 Q8VEA0 | Q8VEA0 mus musculu |
| 19 | 295   | 48.0 | 613 | 4 Q8WUX4  | Q8WUX4 homo sapien |
| 20 | 294.5 | 48.0 | 116 | 4 Q9UL93  | Q9UL93 homo sapien |
| 21 | 291.5 | 47.5 | 113 | 4 Q9UL90  | Q9UL90 homo sapien |
| 22 | 291.5 | 47.5 | 597 | 4 Q96BB9  | Q96BB9 homo sapien |
| 23 | 290   | 47.2 | 118 | 4 Q9UL72  | Q9UL72 homo sapien |
| 24 | 288.5 | 47.0 | 481 | 11 Q91WT1 | Q91WT1 mus musculu |
| 25 | 287   | 46.7 | 147 | 4 Q9Y509  | Q9Y509 homo sapien |
| 26 | 285   | 46.4 | 118 | 4 Q9UL91  | Q9UL91 homo sapien |
| 27 | 284.5 | 46.3 | 119 | 5 Q9GY22  | Q9GY22 schistosoma |
| 28 | 283   | 46.1 | 145 | 11 Q924P7 | Q924P7 mus musculu |
| 29 | 283   | 46.1 | 145 | 11 Q924R1 | Q924R1 mus musculu |
| 30 | 282   | 45.9 | 145 | 11 Q924R4 | Q924R4 mus musculu |
| 31 | 280.5 | 45.7 | 121 | 4 Q9UL71  | Q9UL71 homo sapien |
| 32 | 280.5 | 45.7 | 486 | 11 Q91Z07 | Q91Z07 mus musculu |
| 33 | 280   | 45.6 | 469 | 11 Q8R3V9 | Q8R3V9 mus musculu |
| 34 | 277   | 45.1 | 124 | 6 Q9N0W6  | Q9N0W6 oryctolagus |
| 35 | 277   | 45.1 | 298 | 11 Q90XF0 | Q90XF0 mus musculu |
| 36 | 276.5 | 45.0 | 117 | 11 Q90XE9 | Q90XE9 mus musculu |
| 37 | 276   | 45.0 | 124 | 6 Q9N0W4  | Q9N0W4 oryctolagus |
| 38 | 276   | 45.0 | 143 | 11 Q924R0 | Q924R0 mus musculu |
| 39 | 276   | 45.0 | 471 | 4 Q8TC77  | Q8TC77 homo sapien |
| 40 | 275.5 | 44.9 | 499 | 4 Q8N5K4  | Q8N5K4 homo sapien |
| 41 | 275   | 44.8 | 494 | 4 Q96K68  | Q96K68 homo sapien |
| 42 | 274.5 | 44.7 | 146 | 11 Q924Q3 | Q924Q3 mus musculu |
| 43 | 274.5 | 44.7 | 473 | 11 Q9DBI4 | Q9DBI4 mus musculu |
| 44 | 274   | 44.6 | 122 | 4 Q9UL84  | Q9UL84 homo sapien |
| 45 | 273.5 | 44.5 | 117 | 11 Q90XF0 | Q90XF0 mus musculu |

# ALIGNMENTS

| RESULT 1              | ID   | Q9UL73   | PRELIMINARY: | PRT: | 119 AA. |
|-----------------------|--|--|--------------|------|---------|
| AC                    | Q9UL73   | 01-MAY-2000 (TREMBLrel. 13, Created)                 |              |      |         |
| DT                    | 01-MAY-2000 (TREMBLrel. 13, Last sequence update)                      |  |              |      |         |
| DT                    | 01-MAR-2003 (TREMBLrel. 23, Last annotation update)                    |  |              |      |         |
| DE                    | Myosin-reactive immunoglobulin heavy chain variable region (Fragment). |  |              |      |         |
| OS                    | Homo sapiens (Human).  |  |              |      |         |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |  |              |      |         |
| OC                    | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.              |  |              |      |         |
| OX                    | NCBI_TaxID=9606;   |  |              |      |         |
| RN                    | [1]  |  |              |      |         |
| RP                    | SEQUENCE FROM N.A.   |  |              |      |         |
| RX                    | MEDLINE=98277139; PubMed=9614934;                                      |  |              |      |         |
| RA                    | Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,             |  |              |      |         |
| RA                    | Young D.C.;  |  |              |      |         |
| RT                    | "Myosin-reactive autoantibodies in rheumatic carditis and normal       |  |              |      |         |
| RT                    | fetus.";   |  |              |      |         |
| RU                    | Clin. Immunol. Immunopathol. 87:184-192(1998).                         |  |              |      |         |
| DR                    | EMBL; AF035041; AA056277.1; -.   |  |              |      |         |
| DR                    | HSSP; P01825; 7EAB.  |  |              |      |         |
| DR                    | InterPro; IPR007110; IG-like.  |  |              |      |         |
| DR                    | InterPro; IPR003006; IG_MHC.   |  |              |      |         |
| DR                    | InterPro; IPR003596; IG_V.   |  |              |      |         |
| DR                    | Pfam; PF00047; Ig_1.   |  |              |      |         |
| DR                    | SMART; SM00406; IGV_1.   |  |              |      |         |
| DR                    | PROSITE; PS50835; IG_LIKE; 1.  |  |              |      |         |
| FT                    | NON_TER  | 1  |              |      |         |
| FT                    | NON_TER  | 119  |              |      |         |
| SQ                    | SEQUENCE   | 119 AA; 13219 MW; 1BDB6B6420EA0BE CRC64;             |              |      |         |
| Query Match           |  | 76.6%; Score 470.5; DB 4; Length 119;                |              |      |         |
| Best Local Similarity |  | 79.3%; Pred. No. 1.2e-41;                            |              |      |         |
| Matches               | 92; Conservative   | 8; Mismatches 11; Indels 5; Gaps 2;                  |              |      |         |
| QY                    | 2  | ESGRGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLWIGLYHSGNTYNSL 61 |              |      |         |

DB 6 ESGPGLVKPSETLSLCTVSGSGSICS--YVMSWIRQPGKGLMWIGYIYSGSTNTYPSL 63  
QY 62 KSRVTMSVDTSKNHSRLSSVTAADTAVYYCARSDG---YTDNMGCGTLVTYSS 114  
DB 64 KSRVTISVDTSKNQPSLKLSTLTAADTAVYFCARLSNMGYPYDYGCGTLVTYSS 119

RESULT 2  
ID 095973 PRELIMINARY; PRT; 150 AA.  
AC 095973;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE V44 heavy chain variable region precursor (Fragment).  
GN IGM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;  
RT "Clonal proliferation of IGM secreting B cell in the synovium of  
RT Behcet's patient with arthritis."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF103795; AAC79084.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 >150 V44 HEAVY CHAIN VARIABLE REGION.  
FT NON\_TER 150 150  
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AATC9 CRC64;

Query Match 76.2%; Score 468; DB 4; Length 150;  
Best Local Similarity 78.8%; Pred. No. 3e-41;  
Matches 89; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSETLSLCTVSGSGSIRSGGYWMSWIRQPGKGLMWIGYIYSGSTNTYPSL 61  
DB 25 ESGPGLVKPSETLSLCTVSGSGSISSTNYWGWIRQPEKGLMWISGLNHSGLDYNPSSL 84

QY 62 KSRVTMSVDTSKNHSRLSSVTAADTAVYYCARSDGYTLDNMGCGTLVTYSS 114  
DB 85 KSRVTISVDTSKNQPSLKLSTLTAADTAVYFCARLSNMGYPYDYGCGTLVTYSS 137

RESULT 3  
ID 096KX8 PRELIMINARY; PRT; 496 AA.  
AC 096KX8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Straussberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016369; AAH16369.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 74.9%; Score 460; DB 4; Length 496;  
Best Local Similarity 75.0%; Pred. No. 9.2e-40;  
Matches 90; Conservative 8; Mismatches 14; Indels 8; Gaps 2;

QY 2 ESGPGLVKPSETLSLCTVSGSGSIRSGGYWMSWIRQPGKGLMWIGYIYSGSTNTYPSL 61  
DB 25 ESGPGLVKPSETLSLCTVSGSGSISSTNYWGWIRQPEKGLMWIGYIYSGSTNTYPSL 84

QY 62 KSRVTMSVDTSKNHSRLSSVTAADTAVYYCARSDGYT-----LDNMGCGTLVTYSS 114  
DB 85 KSRVTISVDTSKNQPSLKLSTLTAADTAVYFCAR-HGYSRSGRTGADYWGCGTLVTYSS 143

RESULT 4  
ID 096EY0 PRELIMINARY; PRT; 613 AA.  
AC 096EY0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Straussberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; AAH11857.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 74.9%; Score 460; DB 4; Length 613;  
Best Local Similarity 80.5%; Pred. No. 1.2e-39;  
Matches 95; Conservative 4; Mismatches 11; Indels 8; Gaps 3;

QY 2 ESGPGLVKPSETLSLCTVSGSGSIRSGGYWMSWIRQPGKGLMWIGYIYSGSTNTYPSL 61  
DB 25 ESGPGLVKPSETLSLCTVSGSGSIS--YVMSWIRQPGKGLMWIGYIYSGSTNTYPSL 82

QY 62 KSRVTMSVDTSKNHSRLSSVTAADTAVYYCARSDGYTLDN-----WCGSTLYTVSS 114  
DB 83 KSRVTMSVDTSKNQPSLKLSTLTAADTAVYCA-SQPWELPYVGLFYWGCGTLVTYSS 139

RESULT 5  
ID 081ZD7 PRELIMINARY; PRT; 130 AA.  
AC 081ZD7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Anti-tyroglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.



NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
Jang Y.-U., Chung J., Park J.-Y.,  
"Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-  
Thyroglobulin Single Chain Fv from SLE Patient by Phage Display."  
Submitted (Aug-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AY145445; AA: NC4329.1; -.  
FT NON TER 1  
FT NON TER 130  
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;  
Query Match 70.0%; Score 431; DB 4; Length 130;  
Best Local Similarity 71.2%; Pred. No. 1.9e-37;  
Matches 89; Conservative 8; Mismatches 16; Indels 12; Gaps 4;  
Qy 2 EGGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNT-----Y 56  
Db 6 QGGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTSGSPY 65  
Qy 57 YNPSLKSRVTMSVDTSKNHFSLRLSSVTAADTAAYYCAR---SDG--YT-LDNWGQCTL 109  
Db 66 YAPSLRSVITSVDTSKNQLSLRLSSVTAADTAAYYCARPTHCGGCGCAFFOHWGQGF 125  
Qy 110 VTWSS 114  
Db 126 VTWSS 130  
RESULT 6  
ID Q9WUX4 PRELIMINARY; PRT; 588 AA.  
AC Q9WUX4;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strauberg R.;  
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: BC019235; AA: H19235.1; -.  
DR InterPro: IPR007110; IG\_LIKE.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG\_5.  
DR SMART: SM00406; IG\_1.  
DR PROSITE: PS50835; IG\_LIKE; 5.  
DR PROSITE: PS00290; IG\_MHC; 3.  
KM Hypothetical protein.  
SQ SEQUENCE 588 AA; 64438 MW; F6C0BADA82B3FD7 CRC64;  
Query Match 70.0%; Score 429.5; DB 4; Length 588;  
Best Local Similarity 72.5%; Pred. No. 1.8e-36;  
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;  
Qy 4 GPGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYNNPSLKS 63  
Db 27 GAGGLKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYNNPSLKS 84  
Qy 64 RVTMSVDTSKNHFSLRLSSVTAADTAAYYCAR-----SDG--YT-LDNWGQCTLVTWSS 114  
Db 85 RVTISVDTSKNQLSLRLSSVTAADTAAYYCARPTHCGGCGCAFFOHWGQGF 144  
RESULT 7  
ID Q9BU10 PRELIMINARY; PRT; 597 AA.  
AC Q9BU10;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strauberg R.;  
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: BC002963; AA: H02963.1; -.  
DR HSSP: P01825; F8AB.  
DR InterPro: IPR007110; IG\_LIKE.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG\_5.  
DR SMART: SM00406; IG\_1.  
DR PROSITE: PS50835; IG\_LIKE; 5.  
DR PROSITE: PS00290; IG\_MHC; 3.  
KM Hypothetical protein.  
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;  
Query Match 70.0%; Score 429.5; DB 4; Length 597;  
Best Local Similarity 72.5%; Pred. No. 1.8e-36;  
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;  
Qy 4 GPGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYNNPSLKS 63  
Db 27 GAGGLKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYNNPSLKS 84  
Qy 64 RVTMSVDTSKNHFSLRLSSVTAADTAAYYCAR-----SDG--YT-LDNWGQCTLVTWSS 114  
Db 85 RVTISVDTSKNQLSLRLSSVTAADTAAYYCARPTHCGGCGCAFFOHWGQGF 144  
RESULT 8  
ID Q96AA6 PRELIMINARY; PRT; 618 AA.  
AC Q96AA6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strauberg R.;  
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: BC017356; AA: H17356.1; -.  
DR InterPro: IPR007110; IG\_LIKE.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG\_5.  
DR SMART: SM00406; IG\_1.  
DR PROSITE: PS50835; IG\_LIKE; 5.  
DR PROSITE: PS00290; IG\_MHC; 3.  
KM Hypothetical protein.  
SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C69E0A6 CRC64;  
Query Match 70.0%; Score 429.5; DB 4; Length 618;  
Best Local Similarity 72.5%; Pred. No. 1.9e-36;  
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;  
Qy 4 GPGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYNNPSLKS 63  
Db 27 GAGGLKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLGEMIGIYHSGNTYNNPSLKS 84  
Qy 64 RVTMSVDTSKNHFSLRLSSVTAADTAAYYCAR-----SDG--YT-LDNWGQCTLVTWSS 114  
Db 85 RVTISVDTSKNQLSLRLSSVTAADTAAYYCARPTHCGGCGCAFFOHWGQGF 144

Db 27 GAGLKPSETLSLTCVGGSS--SGYWMIRQPPGKLEWIGELINHSOSTYNNPSLKS 84  
 QY 64 RVTMSVDTSKNHSLSLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 114  
 DB 85 RVTISVDTSKKQLSLKLSVNAADTAVYCARVITRASPGTDGRYGMVDWGCGTIVTVSS 144

## RESULT 9

Q9BOB8 PRELIMINARY; PRT; 597 AA.  
 ID 09BOB8  
 AC 09BOB8; 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle, and Lymph;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC006180; AAH06180.1; -  
 DR EMBL; BC001872; AAH01872.1; -  
 DR HSSP; P01825; 7PAB.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 69.3%; Score 425.5; DB 4; Length 597;  
 Best Local Similarity 72.5%; Pred. No. 4; ee-36;  
 Matches 87; Conservative 6; Mismatches 16; Indels 11; Gaps 3;

QY 4 GPGLVKPSQTLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSLKS 63  
 DB 27 GAGLKPSETLSLTCVGGSS--SGYWMIRQPPGKLEWIGELINHSOSTYNNPSLKS 84  
 QY 64 RVTMSVDTSKNHSLSLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 114  
 DB 85 RVTISVDTSKKQLSLKLSVNAADTAVYCARVITRASPGTDGRYGMVDWGCGTIVTVSS 144

## RESULT 10

Q8TC63 PRELIMINARY; PRT; 473 AA.  
 ID 08TC63  
 AC 08TC63; 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025985; AAH25985.1; -  
 DR InterPro; IPR000923; BlueCu\_1.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 4.

DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0196; COPPER BLUE; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 67.1%; Score 412; DB 4; Length 473;  
 Best Local Similarity 69.0%; Pred. No. 9; ee-35;  
 Matches 80; Conservative 11; Mismatches 19; Indels 6; Gaps 2;

QY 2 ESGPGLVKSQTLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 61  
 DB 32 ESGPGLVKSQTLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 91  
 QY 62 KSRVMSVDTSKNHSLSLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 113  
 DB 92 RSRVMSVDTSKNHSLSLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 145

## RESULT 11

Q99M22 PRELIMINARY; PRT; 479 AA.  
 ID 099M22  
 AC 099M22; 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 52.0 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002091; AAH02091.1; -  
 DR HSSP; P01810; 2FBD.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 63.9%; Score 392.5; DB 11; Length 479;  
 Best Local Similarity 67.5%; Pred. No. 1e-32;  
 Matches 77; Conservative 16; Mismatches 18; Indels 3; Gaps 3;

QY 2 ESGPGLVKSQTLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 61  
 DB 24 ESGPGLVKSQTLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 82  
 QY 62 KSRVMSVDTSKNHSLSLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 114  
 DB 83 KSRVMSVDTSKNHSLSLSTCTVSGGSGIRSGYWMIRQPPGKLEWIGELINHSOSTYNNPSL 135

## RESULT 12

Q9UL75 PRELIMINARY; PRT; 122 AA.  
 ID 09UL75  
 AC 09UL75; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL  fetus.";
DR  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035018; AAD56275.1; -.
DR  HSSP; P01825; 7FAB.
DR  InterPro; IPR007110; IG_1like.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
FT  NON_TER
FT  NON_TER
SQ  SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match
Best Local Similarity 59.3%; Score 364; DB 4; Length 122;
Matches 72; Conservative 13; Mismatches 28; Indels 4; Gaps 2;

OY  2 ESGPGLVPSQTLSTICTVSGSIRSGGYMSWIRPPGKGLWIGYIHSGNTY--YNP 59
DB  6 QSGPGLVPSQTLSTICTAISGDSVSSNSAMWMIQSPRGLWIGRTYRSKWYNDYRV 65

OY  60 SLKRVTSVDPSTSKHPSLRSLSSVTADTAAYVYCARSDGY--TLDMNGGTLVTVSS 114
DB  66 SVKSRITINPDTSKQPSLQNLNSVTPEDTAAYVYCARDELGLQGFYWGQGITLVTVSS 122

RESULT 13
OY  96 PRELIMINARY; PRT; 121 AA.
AC  Q9UL96
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Myosin-reactive immunoglobulin heavy chain variable region
DE  (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL  fetus.";
DR  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035018; AAD56254.1; -.
DR  HSSP; P01825; 7FAB.
DR  InterPro; IPR007110; IG_1like.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
FT  NON_TER
FT  NON_TER
SQ  SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match
Best Local Similarity 56.1%; Score 344.5; DB 4; Length 121;
Matches 68; Conservative 13; Mismatches 32; Indels 3; Gaps 1;

OY  2 ESGPGLVPSQTLSTICTVSGSIRSGGYMSWIRPPGKGLWIGYIHSGNTYNSL 61
DB  66 SVKSRITINPDTSKQPSLQNLNSVTPEDTAAYVYCARDELGLQGFYWGQGITLVTVSS 122
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DB  6 ESGPGLVPSQTLSTICTVSGSIRSGMDVGMIRPPGKGLWIALIYDDDKRYSBSL 65

OY  62 KSRVTMSVDTSKHPSLRSLSSVTADTAAYVYCAR---SDGTLDMNGGTLVTVSS 114
DB  66 KSRITITKDTSKNOVDLTMTFMDPWDTATYVYCARKSGDGYFDFYWGQGITLVTVSS 121

RESULT 14
OY  96 PRELIMINARY; PRT; 121 AA.
AC  Q99NG4
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Single chain Fv (Fragment).
OS  Mus musculus (Mouse).
OC  Plasmid PHEN1.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/C;
RX  MEDLINE=98169018; PubMed=9510199;
RA  Hawlisch H., Frank R., Hennecke M., Baensch M., Sohne B., Arseniev L.,
RA  Baetsch W., Kola A., Kios A., Koehl J.,
RT  "Site-directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL  J. Immunol. 160:2947-2958(1998).
DR  EMBL; AJ222590; CAA10890.1; -.
DR  HSSP; P01825; 7FAB.
DR  InterPro; IPR007110; IG_1like.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Plasmid.
FT  NON_TER
FT  NON_TER
SQ  SEQUENCE 121 AA; 13255 MW; D293E4EBC8C9D5B CRC64;

Query Match
Best Local Similarity 55.4%; Score 340; DB 11; Length 121;
Matches 68; Conservative 16; Mismatches 27; Indels 6; Gaps 2;

OY  2 ESGPGLVPSQTLSTICTVSGSIRSGGYMSWIRPPGKGLWIGYIHSGNTYNSL 61
DB  6 ESGPGLVPSQTLSTICTVSGFPLTSHGV--SWVRQPPGKGLWIGYIWGDGNTKYHSAL 63

OY  62 KSRVTMSVDTSKHPSLRSLSSVTADTAAYVYCAR---DGYTLDMNGGTLVTVSS 114
DB  64 ISRLSKDNKSKOVFLKNSLQTEDTATYVYCARHYRYKANYAMDYWGQGSTVTVSS 120

RESULT 15
OY  96 PRELIMINARY; PRT; 482 AA.
AC  Q91X92
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Unknown (Protein for WGC:18822).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Colon;
RA  Strausberg R.,
RT  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL  EMBL; BC011181; AAH11181.1; -.
DR  InterPro; IPR007110; IG_1like.
```

DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF0047; IG; 4.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS00835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; 2.  
SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;

Query Match 54.7%; Score 336; DB 11; Length 482;  
Best Local Similarity 58.3%; Pred. No. 8.6e-27;  
Matches 67; Conservative 17; Mismatches 27; Indels 4; Gaps 2;

QY 2 ESGPGIVKPSQTLSTCTVSGGSIKSGYVSWIRQPGKGLWIGYIYHSGNTYNPSTL 61  
Db 25 ESGPDLVAPQSLSITCTVSGFALTS--YAIISWVRQPGKGLWIGVITGVTNYSAL 82  
QY 62 KSRVTWSVDTSKNHFSLRLSVYAADTAVYCARSDGY--TLDNMGQTLVTYSS 114  
Db 83 KSRLSISKNSKSKSQVFLKNLSLOTNTARYCARSDSNYEGAMDYWGQTSVTYSS 137

Search completed: February 10, 2004, 18:39:21  
Job time : 27.9455 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:46:18 ; Search time 34.3727 Seconds  
(without alignments)  
526.430 Million cell updates/sec

Title: US-10-027-725A-9  
Perfect score: 614  
Sequence: 1 LBSGPGLVKSQTLSTLCTV.....RSDGYTLDMQGLTVYSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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| 3:  | /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:* |
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| 23: | /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:* |
| 24: | /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 605   | 98.5        | 114    | 23 | ABG30447    |
| 2          | 600   | 97.7        | 114    | 23 | ABG30446    |
| 3          | 556   | 90.6        | 114    | 23 | ABG30445    |
| 4          | 521   | 84.9        | 473    | 22 | ABR36206    |
| 5          | 516.5 | 84.1        | 123    | 20 | AAW78433    |
| 6          | 516.5 | 84.1        | 123    | 23 | ABR97976    |
| 7          | 513.5 | 83.6        | 120    | 22 | ABR62775    |
| 8          | 512   | 83.4        | 123    | 22 | ABR62745    |
| 9          | 510.5 | 83.1        | 122    | 22 | ABR62765    |

|    |       |      |     |    |           |
|----|-------|------|-----|----|-----------|
| 10 | 510   | 83.1 | 246 | 21 | AAV15126  |
| 11 | 508   | 82.7 | 172 | 21 | AAV93713  |
| 12 | 507   | 82.6 | 126 | 21 | AAH30584  |
| 13 | 507   | 82.6 | 126 | 23 | ABP54970  |
| 14 | 507   | 82.6 | 251 | 23 | ABG80712  |
| 15 | 507   | 82.6 | 252 | 23 | ABP45963  |
| 16 | 507   | 82.6 | 254 | 23 | ABG80713  |
| 17 | 507   | 82.6 | 263 | 23 | ABG80714  |
| 18 | 506.5 | 82.5 | 251 | 24 | ABJ19839  |
| 19 | 506.5 | 82.5 | 253 | 23 | ABP45608  |
| 20 | 503   | 81.9 | 252 | 23 | ABP45318  |
| 21 | 502.5 | 81.8 | 119 | 18 | AAW27554  |
| 22 | 502.5 | 81.8 | 119 | 24 | ABJ18676  |
| 23 | 502.5 | 81.8 | 127 | 22 | AAAG80217 |
| 24 | 502   | 81.8 | 118 | 20 | AAV06385  |
| 25 | 502   | 81.8 | 139 | 21 | AAV56713  |
| 26 | 501   | 81.6 | 130 | 23 | AAU81273  |
| 27 | 501   | 81.6 | 256 | 23 | ABP45596  |
| 28 | 496   | 80.8 | 121 | 23 | ABR07171  |
| 29 | 495.5 | 80.7 | 129 | 23 | AAU81275  |
| 30 | 495   | 80.6 | 118 | 20 | AAV06383  |
| 31 | 494.5 | 80.5 | 251 | 23 | ABP44979  |
| 32 | 492.5 | 80.2 | 117 | 21 | AAV44615  |
| 33 | 492   | 80.1 | 487 | 22 | ABR90607  |
| 34 | 492   | 80.1 | 487 | 23 | ABG65445  |
| 35 | 491.5 | 80.0 | 120 | 23 | AAU81276  |
| 36 | 491   | 80.0 | 129 | 20 | AAH90287  |
| 37 | 490   | 79.8 | 229 | 21 | AAH30593  |
| 38 | 489   | 79.6 | 118 | 20 | AAV06386  |
| 39 | 489   | 79.6 | 126 | 23 | ABG92888  |
| 40 | 487.5 | 79.4 | 119 | 24 | AAH30143  |
| 41 | 487.5 | 79.4 | 119 | 14 | ABP98683  |
| 42 | 487.5 | 79.4 | 119 | 24 | ABP98691  |
| 43 | 486   | 79.2 | 117 | 22 | AAU02540  |
| 44 | 486   | 79.2 | 122 | 14 | AAH30145  |
| 45 | 485   | 79.0 | 139 | 21 | AAV82628  |

## ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| ID       | ABG30447 standard; Protein; 114 AA.                       |
| AC       | ABG30447;   |
| XX       |   |
| XX       |   |
| DT       | 21-OCT-2002 (first entry)                                 |
| DE       | Human IGE Fab clone 100 heavy chain protein.              |
| XX       |   |
| XX       |   |
| KW       | Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2 |
| KW       | timothy grass pollen allergen; passive immunotherapy.     |
| XX       |   |
| OS       | Homo sapiens.   |
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| FT       | Region  |
| FT       |   |
| FT       | Region  |
| FT       |   |
| FT       | Region  |
| FT       | </  |

Anti-murine CTLA-4  
The heavy chain of  
A human variable h  
Anti-idiotypic VH  
Amyloid peptide co  
Human Blys binding  
Amyloid peptide co  
Human IGF/factor X  
Human VEGF-2 relat  
Human Blys binding  
Human Blys binding  
Human Ab heavy cha  
Antibody library r  
Human autoantibody  
Humanised IM609 an  
Amino acid sequenc  
Human tTcC antibod  
Human Blys binding  
Human Blys binding  
ebvH1GM MS119D10 h  
Human tTcC antibod  
Humanised IM609 an  
Human Blys binding  
Human antibody clo  
Human secreted pro  
Human albumin fusi  
Human tTcC antibod  
Human anti-GR1b/I  
Variable and first  
Humanised IM609 an  
Human immunoglobul  
Mab GAH variable r  
Human GAH antibody  
Human GAH antibody  
Anti-adipocyte mon  
Mab 1-3-1 variable  
Human PTHrP monocl

XX 11-JUL-2002.  
 PD 27-DEC-2001; 2001WO-SE02908.  
 XX 29-DEC-2000; 2000SE-0004892.  
 XX (PHMA ) PHARMACIA DIAGNOSTICS AB.  
 XX Flicker S, Steindberger P, Kraft D, Valenta R,  
 PI N-PSDB; ABRK9639.  
 DR WPI; 2002-583604/62.  
 XX  
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for  
 PT environmental allergen detection -  
 XX  
 PS Disclosure; Page 38; 45pp; English.  
 CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's  
 CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).  
 CC The group 2 allergen-specific Fabs of the invention may be useful for  
 CC environmental allergen detection and for standardisation of allergen  
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for  
 CC passive immunotherapy of type I allergy, it is also useful for  
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention  
 CC are useful for inter alia, diagnosis, therapy and prevention of type  
 CC I allergy. They are also useful for identification of group 2  
 CC allergen-containing pollen and may be used for blocking the binding of  
 CC grass pollen allergic patients IgE antibodies to Phi p 2. The present  
 CC sequence represents the human IgG fab, clone 100 heavy chain protein of  
 CC the invention.  
 XX  
 SO Sequence 114 AA;  
 Query Match 98.5%; Score 605; DB 23; Length 114;  
 Best Local Similarity 99.1%; Pred. No. 1.4e-44;  
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPKGLKLEWIGYIYHSGNTYYNS 60  
 DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPKGLKLEWIGYIYHSGNTYYNS 60  
 QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAIVYVCARSDGYTLDMWGGTLVTYSS 114  
 DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAIVYVCARSDGYTLDMWGGTLVTYSS 114  
 RESULT 2  
 ABG30446  
 ID ABG30446 standard; Protein; 114 AA.  
 XX  
 AC ABG30446;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human IgE Fab clone 60 heavy chain protein.  
 XX  
 KW Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;  
 XX timothy grass pollen allergen; passive immunotherapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..26  
 FT /note= "FRI region"  
 FT 27..33  
 FT Region /note= "CDRI region"

FT Region 34..47  
 FT /note= "FR2 region"  
 FT Region 48..63  
 FT /note= "CDR2 protein"  
 FT Region 64..95  
 FT /note= "FR3 region"  
 FT Region 96..103  
 FT /note= "CDR2 region"  
 FT Region 104..114  
 FT /note= "FR4 region"  
 XX  
 XX WO200253595-A1.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 27-DEC-2001; 2001WO-SE02908.  
 XX  
 PR 29-DEC-2000; 2000SE-0004892.  
 XX  
 XX (PHMA ) PHARMACIA DIAGNOSTICS AB.  
 XX Flicker S, Steindberger P, Kraft D, Valenta R,  
 PI N-PSDB; ABRK9638.  
 DR WPI; 2002-583604/62.  
 XX  
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for  
 PT environmental allergen detection -  
 XX  
 PS Disclosure; Page 37; 45pp; English.  
 CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's  
 CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).  
 CC The group 2 allergen-specific Fabs of the invention may be useful for  
 CC environmental allergen detection and for standardisation of allergen  
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for  
 CC passive immunotherapy of type I allergy, it is also useful for  
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention  
 CC are useful for inter alia, diagnosis, therapy and prevention of type  
 CC I allergy. They are also useful for identification of group 2  
 CC allergen-containing pollen and may be used for blocking the binding of  
 CC grass pollen allergic patients IgE antibodies to Phi p 2. The present  
 CC sequence represents the human IgG fab, clone 60 heavy chain protein of  
 CC the invention.  
 XX  
 SO Sequence 114 AA;  
 Query Match 97.7%; Score 600; DB 23; Length 114;  
 Best Local Similarity 96.5%; Pred. No. 3.8e-44;  
 Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPKGLKLEWIGYIYHSGNTYYNS 60  
 DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPKGLKLEWIGYIYHSGNTYYNS 60  
 QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAIVYVCARSDGYTLDMWGGTLVTYSS 114  
 DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAIVYVCARSDGYTLDMWGGTLVTYSS 114  
 RESULT 3  
 ABG30445  
 ID ABG30445 standard; Protein; 114 AA.  
 XX  
 AC ABG30445;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX

DE Human IGE Fab clone 94 heavy chain protein.  
 XX  
 KW Human; fab; anti allergic; vaccine; grass pollen; Phi p 2;  
 KW Timothy grass pollen allergen; passive immunotherapy.  
 XX  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 FH Region 1..26  
 FT /note= "FR1 region"  
 FT Region 27..33  
 FT /note= "CDR1 region"  
 FT Region 34..47  
 FT /note= "FR2 region"  
 FT Region 48..63  
 FT /note= "CDR2 protein"  
 FT Region 64..95  
 FT /note= "FR3 region"  
 FT Region 96..103  
 FT /note= "CDR2 region"  
 FT Region 104..114  
 FT /note= "FR4 region"  
 PN WO200253595-A1.  
 PD 11-JUL-2002.  
 XX  
 PD 27-DEC-2001; 2001WO-SE02908.  
 XX  
 PD 29-DEC-2000; 2000SE-0004892.  
 PR (PHAA ) PHARMACIA DIAGNOSTICS AB.  
 PA  
 PI Flicker S, Steinberger P, Kraft D, Valenta R;  
 XX  
 XX WPI: 2002-583604/62.  
 DR N-PSDB; ABK89637.  
 XX  
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IGE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for  
 PT environmental allergen detection -  
 XX  
 XX Disclosure; Page 36; 45pp; English.  
 PS  
 XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IGE Fabs and methods for their use. The proteins  
 CC of the invention may have anti allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's  
 CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).  
 CC The group 2 allergen-specific fabs of the invention may be useful for  
 CC environmental allergen detection and for standardisation of allergen  
 CC extracts. The fabs - or a vaccine against a type I allergy is useful for  
 CC passive immunotherapy of type I allergy; it is also useful for  
 CC diagnosing a type I allergy. The allergen-specific fabs of the invention  
 CC are useful for inter alia, diagnosis, therapy and prevention of type  
 CC I allergy. They are also useful for identification of group 2  
 CC allergen-containing pollen and may be used for blocking the binding of  
 CC grass pollen allergic patients IGE antibodies to Phi p 2. The present  
 CC sequence represents the human IGE fab, clone 94 heavy chain protein of  
 CC the invention.  
 CC  
 XX  
 XX Sequence 114 AA;  
 SQ  
 Query Match 90.6%; Score 556; DB 23; Length 114;  
 Best Local Similarity 90.4%; Pred. No. 2.2e-40;  
 Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 LESGPGALVKKPQSLTSLCTVSGSGSIRSGGYWMSWIRQPPGKGLWIGYIHSGNTYVNS 60  
 DB 1 LESGPGALVKKPQSLTSLCTVSGSGSIRSGGYWMSWIRQPPGKGLWIGYIHSGNTYVNS 60  
 QY 1 LKSRVMSVDTSKNHFSLRLSSVTAADTAIVYYCARSDGYTLTDNMGGTLVTVSS 114

[illegible]

DE Antibody heavy chain targeted to obr clone 26.  
XX  
XX Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;  
KW diagnosis; cancer; primer; PCR; amplification; diagnostic.  
XX  
XX Synthetic.  
XX  
XX MO9850431-A2.  
XX  
XX 12-NOV-1998.  
XX  
XX 30-APR-1998; 98MO-US08762.  
XX  
XX 24-JUN-1997; 97US-0050661.  
PR 02-MAY-1997; 97US-0850058.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Arathoon R, Carter PJ, Merchant AM, Presta LG;  
PI WPI; 1999-070091/06.  
XX  
XX Selective preparation of multispecific antibodies - with  
PT heteromultimeric heavy chain and common light chain components,  
PT useful for, e.g. in vivo diagnosis of cancer  
XX  
XX Example 4; Fig 5; 69pp; English.  
XX  
XX This sequence represents the heavy chain variable region for an antibody  
CC that binds to the obr clone 26 protein. The sequence encoding the chain  
CC is generated by a new method for preparing a multispecific Ab comprising  
CC a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP  
CC comprises a multimerisation domain (MD) forming an interface positioned  
CC to interact with an interface of a MD of the extra PP; and (ii) the first  
CC and extra PPs each have a binding domain, which comprises a heavy chain  
CC and a light chain, where the variable light chains of the first and extra  
CC PPs comprise a common sequence. The method comprises: (a) culturing a  
CC host cell comprising nucleic acid encoding the first PP and extra PP, and  
CC the variable light chain, such that the nucleic acid is expressed; and  
CC (b) recovering the multispecific Ab from the culture. The method prepares  
CC heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins  
CC and Ab-immunoadhesin chimeras. The method allows for the enhanced  
CC formation of the desired heteromultimer relative to the undesired  
CC heteromultimers and homomultimers. The Abs can be used in immunoassays  
CC and for the in vitro or in vivo diagnosis of various diseases, such as  
CC cancer.  
XX  
XX  
SQ Sequence 123 AA;  
XX  
XX Query Match 84.1%; Score 516.5; DB 20; Length 123;  
Best Local Similarity 84.0%; Pred. No. 5.8e-37;  
Matches 100; Conservative 5; Mismatches 9; Indels 5; Gaps 1;  
XX  
QY 1 LBSGPGLVKPSQTLSTCTVSGSGISRGYSWIRPGKGLWIGYIHSGNTYNS 60  
DB 5 VBSGPGLVKPSQTLSTCTVSGSGISRGYSWIRPGKGLWIGYIHSGNTYNS 64  
QY 61 LKSRVTMSVDTSKNHSRLSSVTADTAVVYCARSD-----GYTLDMNGGTLTVSS 114  
DB 65 LKSRVTISVDTSKNHSRLSSVTADTAVVYCARVLDLEDYSGASDYMGGTLTVSS 123  
XX  
XX RESULT 6  
ABBS97976  
ID ABB97976 standard; Protein; 123 AA.  
XX  
XX ABB97976;  
AC  
DT 06-SEP-2002 (first entry)  
XX  
XX Heavy chain variable region from antibody obr.26.  
DE  
XX Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;  
XX

KW antiviral; vaccine; tumour.  
XX  
XX Synthetic.  
XX  
XX US2002062010-A1.  
XX  
XX 23-MAY-2002.  
XX  
XX 23-MAY-2001; 2001US-0863693.  
XX  
XX 02-MAY-1997; 97US-046816P.  
PR 30-APR-1998; 98US-0070166.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Arathoon WR, Carter PJ, Merchant AM, Presta LG;  
PI WPI; 2002-499676/53.  
XX  
XX New multispecific antibodies having heteromultimeric and common  
PT components are useful to direct treatment to a target site such as a  
PT tumour cell, cell surface receptor or clot, as a vaccine adjuvant and to  
PT treat infectious disease  
XX  
XX Example 4; Fig 5; 36pp; English.  
XX  
XX The invention relates to a new multispecific antibody, comprising at  
CC least two polypeptides (PP1 and PP2) which meet at a multiface, where PP1  
CC has a multimerisation domain forming an interface positioned to interact  
CC with an interface of a multimerisation domain of PP2, and both  
CC polypeptides each comprise a binding domain consisting a heavy chain and  
CC a variable light chain, where the light chain has a sequence common to  
CC both polypeptides. Heteromultimers of the inventions include bispecific  
CC antibodies, bispecific immunoadhesins and antibody-immunoadhesin  
CC chimeras. The activity of antibodies of the invention may be described  
CC as, cytostatic, antibacterial and antiviral. The heteromultimer  
CC can be used for redirected cytotoxicity, for example to kill tumour  
CC cells, as a vaccine adjuvant, for delivering thrombolytic agents to  
CC clots, for converting enzyme activated prodrugs at a target site such as  
CC a tumour, for treating infectious diseases, for targeting immune  
CC complexes to cell surface receptors or for delivering immunotoxins to  
CC tumour cells. The current sequence represents the heavy chain variable  
CC region from antibody obr.26 used in the construction of bispecific  
CC antibodies.  
XX  
XX  
SQ Sequence 123 AA;  
XX  
XX Query Match 84.1%; Score 516.5; DB 23; Length 123;  
Best Local Similarity 84.0%; Pred. No. 5.8e-37;  
Matches 100; Conservative 5; Mismatches 9; Indels 5; Gaps 1;  
XX  
QY 1 LBSGPGLVKPSQTLSTCTVSGSGISRGYSWIRPGKGLWIGYIHSGNTYNS 60  
DB 5 VBSGPGLVKPSQTLSTCTVSGSGISRGYSWIRPGKGLWIGYIHSGNTYNS 64  
QY 61 LKSRVTMSVDTSKNHSRLSSVTADTAVVYCARSD-----GYTLDMNGGTLTVSS 114  
DB 65 LKSRVTISVDTSKNHSRLSSVTADTAVVYCARVLDLEDYSGASDYMGGTLTVSS 123  
XX  
XX RESULT 7  
AAB62775  
ID AAB62775 standard; Protein; 120 AA.  
XX  
XX AAB62775;  
AC  
DT 03-APR-2001 (first entry)  
XX  
XX Human HIV-1 monoclonal antibody SEQ ID NO: 74.  
DE  
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
KW envelope glycoprotein; gp120; diagnosis.  
XX



|          |   |
|----------|---|
| XX       | Homo sapiens.   |
| PN       | WO20010678-A1.  |
| PD       | 04-JAN-2001.  |
| PF       | 23-JUN-2000; 2000WO-US17327.  |
| PR       | 30-JUN-1999; 99US-0141701.  |
| PA       | (USSH ) US DEPT HEALTH & HUMAN SERVICES.  |
| PI       | Mackins BA, Reitz MS;   |
| DR       | WPI; 2001-112438/12.  |
| DR       | N-PSDB; AAF29076.   |
| XX       | Novel human monoclonal antibody immunoreactive with human<br>immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1<br>in biological sample and providing passive immunotherapy for HIV-1<br>infected mammal -   |
| XS       | Claim 1; Page 69; 81pp; English.  |
| CC       | The present invention provides the protein and coding sequences for the<br>variable regions of human monoclonal antibodies which are immunoreactive<br>with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.<br>These can be used in diagnosis and therapy of HIV-1 infection. |
| Sequence | 120 AA;   |

|                           |       |                 |          |            |
|---------------------------|-------|-----------------|----------|------------|
| Query Match               | 83.6% | Score 513.5     | DB 22    | Length 120 |
| Best Local Similarity     | 86.2% | Pred. No. 1e-36 |          |            |
| Matches 100, Conservative | 5     | Mismatches 6    | Indels 5 | Gaps 2     |

Qy 2 ESAGGLVAPSGTTSLTCTVSGSGSLRSGGYWSWIRPGPGKGLMEIGYIYSSGNTYNNPSL 61  
 Db 7 ESAGGLVAPSGTTSLTCTVSGSGSLSSGGYWSWIRQHPGKGLMEIGYIYSSGTYNNPSL 66  
 Qy 62 KSRVTMSVDTSKMFSLRLSSVTYADPAVYVCARS--DGYLDNMGQGTLYVYSS 114  
 Db 67 KSRVTISVDTSKMFSLRLSSVTYADPAVYVCAGVVDMF--DPMGQGTLYVYSS 120

RESULT 8  
AAB62745  
ID AAB62745 standard; Protein; 123 AA

|    |  |               |
|----|--|---------------|
| DT | 03-APR-2001  | (first entry) |
| XX |  |               |
| DE | Human HIV-1 monoclonal antibody SEQ ID NO: 44.                   |               |
| XX |  |               |
| KM | Human immunodeficiency virus-1, HIV-1; human monoclonal antibody |               |
| KM | envelope glycoprotein; gp120; diagnosis.                         |               |
| XX |  |               |
| OS | Homo sapiens.  |               |
| XX |  |               |
| PN | WO20010678-A1.   |               |
| PD | 04-JAN-2001.   |               |
| XX |  |               |
| PF | 23-JUN-2000; 2000WO-US17327.                                     |               |
| XX |  |               |
| PR | 30-JUN-1999; 99US-0141701.                                       |               |
| XX |  |               |
| PA | (USSH ) US DEPT HEALTH & HUMAN SERVICES.                         |               |
| XX |  |               |
| PI | Watkins BA, Reitz MS;  |               |
| DR | WPI; 2001-112438/12.   |               |
| DR | N-PSDB; AAF29046.  |               |

XX Novel human monoclonal antibody immunoreactive with human  
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
PT in biological sample and providing passive immunotherapy to HIV-1  
PT infected mammal -  
XX  
XX  
PS Claim 1, Page 50, 81pp; English.  
XX  
XX The present invention provides the protein and coding sequences for the  
CC variable regions of human monoclonal antibodies which are immunoreactive  
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
CC These can be used in diagnosis and therapy of HIV-1 infection.  
XX  
XX Sequence 123 AA;

|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 83.4%          | Score 512         | DB 22    | Length 123 |
| Best Local Similarity | 83.8%          | Pred. No. 1.4e-35 |          |            |
| Matches 98            | Conservative 7 | Mismatches 8      | Indels 4 | Gaps 1     |

Qy 2 ESAGGLVAKPQSTLSLCTCTGSGGIRSGGGYVMSVIRPPPKGLGEMIGYIHSNGTAYNPGL 61  
Db 7 ESERGLVAKPQSTLSLCTCTGSGGISGSGGYVMSVIRHPKGLGEMIGYIHSNGSTYNNPGL 66  
Qy 62 KSRVTMSVDTSKNHFSLRLSTVADPNTAYYICAR----DGYTLNMGCGTLVYSS 114  
Db 67 KSRVTISIDTSKNKFKLSSTVADPNTAYYICARAYVCGDGSFDWGGGTLVYSS 123

RESULT 9  
AAB62765  
ID AAB62765 standard; Protein; 122 AA

DT 03-APR-2001 (first entry

DE Human HIV-1 monoclonal antibody SEQ ID NO: 64

KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody,  
envelope glycoprotein; gp120; diagnosis.

OS Homo sapiens

PN WO200100678-A1

PD 04-JAN-2001

23-JUN-2000; 2000WO-US17327.

AA 30-JUN-1999; 99US-0141701.  
PR

AA (USSH ) US DEPT HEALTH & HUMAN SERVICES  
PA

Watkins BA, Reitz MS; PI

WPI; 2001-112438/12.

PT Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1 infected mammal -

PS Claim 1; Page 63; 81pp; English

CC The present invention provides the protein and coding sequences for the  
CC variable regions of human monoclonal antibodies which are immunoreactive  
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
CC These can be used in diagnosis and therapy of HIV-1 infection.

Query Match 83.1%; Score 510.5; DB 22; Length 122;

Best Local Similarity 85.3%; Pred. No. 1.9e-36;  
Matches 99; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 61  
DB 7 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 66  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLVTYSS 114  
DB 67 KSRVTISVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLVTYSS 122

## RESULT 10

AA15126  
ID AA15126 standard; Protein; 246 AA.

AC AA15126;  
DT 07-FEB-2000 (first entry)  
XX  
DE Anti-murine CTLA-4 M3 sFv.  
XX  
KW Anti-murine CTLA-4 sFv; M3 sFv; single chain antibody; murine CTLA4;  
KW membrane-associated protein; chimeric construct; extracellular domain;  
KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;  
KW recipient CD28; T-cell proliferation;  
KW xenograft-specific immunosuppression.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN MO9957266-A2.  
XX  
PD 11-NOV-1999.  
XX  
PF 30-APR-1999; 99MO-GB01350.  
XX  
PR 30-APR-1998; 98GB-0009280.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Lechler IR, Dorling A;  
XX  
DR MPI: 2000-038815/03.  
XX  
DR N-PSDB; AA228998.  
XX  
PT Inhibiting T-cell mediated rejection of xenotransplanted organs  
XX  
PS Claim 9; Fig 11; 43pp; English.  
XX  
CC The present sequence is the anti-murine CTLA-4 sFv (M3 sFv). This is a  
CC membrane-associated protein which binds to CTLA-4. Chimeric constructs  
CC comprising DNA sequences encoding the extracellular domain of murine  
CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.  
CC The anti-CTLA4 sFv functions as a ligand binding to CTLA-4 on activated  
CC T-cells and antagonises the co-stimulatory signal provided by the  
CC interaction between donor B7 and recipient CD28. Cells expressing the  
CC anti-CTLA4 sFv failed to stimulate T-cell proliferation. This is used in  
CC xenograft-specific immunosuppression.  
XX  
SQ Sequence 246 AA;

Query Match 83.1%; Score 510; DB 21; Length 246;  
Best Local Similarity 85.0%; Pred. No. 4.3e-36;  
Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 61  
DB 8 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 67  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLVTYSS 114  
DB 68 KSRVTISVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLVTYSS 120

## RESULT 11

AA93713  
ID AA93713 standard; Protein; 172 AA.

AC AA93713;  
XX  
DT 03-OCT-2000 (first entry)  
XX  
DE The heavy chain of immunoglobulin clone 2.1.3.  
XX  
KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;  
KW proliferative disorder; cancer; immunodeficient disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200037504-A2.  
XX  
PD 29-JUN-2000.  
XX  
PF 23-DEC-1999; 99MO-US30895.  
XX  
PR 23-DEC-1998; 98US-0113647.  
XX

PA (PFIZ ) PFIZER INC.  
PA (ABGE-) ABGENIX INC.  
XX  
PI Hanson DC, Neveu MJ, Mueller EB, Hanke JH, Gilman SC, Davis CG;  
PI Corvalan JR;  
XX  
DR MPI: 2000-442647/38.  
DR N-PSDB; AAA46876.  
XX  
PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen  
PT (CTLA)-4 containing specified heavy and light chain sequences, useful  
PT for treating, e.g. immune disorders -  
XX  
PS Claim 2; Fig 1G; 157pp; English.  
XX  
CC The present sequence represents a heavy chain of an antibody of the  
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen  
CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain  
CC variable region, comprising a modified contiguous sequence from a  
CC FRI-PR3 sequence encoded by a human VH3-33 family gene. The  
CC modifications are contained in CDR1, CDR2 and/or framework regions.  
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the  
CC immune system to treat hyperimmunity disorders (e.g. autoimmune  
CC disease, diabetes and graft rejection) and proliferative disorders  
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate  
CC immune system to up-regulate immunodeficient disorders.  
XX  
SQ Sequence 172 AA;

Query Match 82.7%; Score 508; DB 21; Length 172;  
Best Local Similarity 85.1%; Pred. No. 4.4e-36;  
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 3 SGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 62  
DB 1 SGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 60  
QY 63 KSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLVTYSS 114  
DB 61 KSRVTISVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLVTYSS 114

## RESULT 12

AA30584  
ID AA30584 standard; Protein; 126 AA.

AC AA30584;

XX 19-MAR-2001 (first entry)  
 DT A human variable heavy chain region of anti-IgE antibody.  
 XX  
 DE Anti-idiotype antibody; C-epsilon3 region; immunoglobulin E; IgE;  
 XX anti-IgE antibody; mimobody; vaccine; allergy; asthma; atopic dermatitis;  
 KW rhinitis; chronic urticaria; food allergy; IgE-mediated disease;  
 KM passive immunisation.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT Region 30..37 /note="complementarity determining region 1"  
 FT Region 51..67 /note="complementarity determining region 2"  
 FT Region 100..115 /note="complementarity determining region 3"  
 FT Region /note="complementarity determining region 3"  
 FT  
 XX WO200063252-A1.  
 EN  
 XX 26-OCT-2000.  
 XX  
 XX 12-APR-2000; 2000WO-BP03288.  
 XX  
 XX 14-APR-1999; 99GB-0008533.  
 XX  
 XX (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-BRFINDUNGEN VERW GES MBH.  
 XX  
 PI Kricek F, Stadler B, Vogel M;  
 XX  
 DR WPI; 2000-687161/67.  
 DR N-PSDB; AAC62336.  
 XX  
 XX Novel anti-idiotypic antibody against antibodies which inhibit binding  
 PT of immunoglobulin E to its high affinity receptor, useful in vaccines  
 PT for treating diseases such as allergy, rhinitis, atopic dermatitis -  
 XX  
 XX Claim 4; Fig 5c; 73pp; English.  
 XX  
 XX The present sequence represents a human variable heavy chain region of  
 CC an anti-idiotype antibody that interferes with the binding of the  
 CC C-epsilon3 region of immunoglobulin (Ig)E to the high affinity receptor  
 CC for IgE, i.e. and anti-IgE antibody. Such an antibody is referred to  
 CC as a mimobody. The anti-IgE antibody fragment is used as a vaccine, and  
 CC as a pharmaceutical for treating IgE-mediated diseases such as allergy,  
 CC in particular asthma, atopic dermatitis, rhinitis, chronic urticaria and  
 CC food allergies. It is also used to treat IgE-mediated diseases. It is  
 CC also used for raising polyclonal or monoclonal antibodies. The polyclonal  
 CC or monoclonal antibodies obtained are useful for treating IgE-mediated  
 CC diseases by passive immunisation.  
 CC  
 XX  
 SQ Sequence 126 AA;  
 Query Match 82.6%; Score 507; DB 21; Length 126;  
 Best Local Similarity 80.3%; Pred. No. 3.9e-36;  
 Matches 98; Conservative 6; Mismatches 10; Indels 8; Gaps 1;  
 QY 1 LESGGLVKSPTSLTCTVSGGSIIRSGYMSWIRPPGKLEWIGIYHSGNTYNNPS 60  
 DB 5 LESGGLVKSPTSLTCTVSGGSIIRSGYMSWIRPPGKLEWIGIYHSGNTYNNPS 64  
 QY 61 LKSRVTMSVDTSKNFSRLTSSVTAADTAAYVYCARSDG-----YTLDNMGCGTLVTV 112  
 DB 65 LKSRVTMSVDTSKNFSRLTSSVTAADTAAYVYCARSDG-----YTLDNMGCGTLVTV 124  
 QY 113 SS 114  
 DB 125 SS 126

RESULT 13  
 ID ABP54970 standard; Protein: 126 AA.  
 XX  
 AC ABP54970;  
 XX  
 DT 14-JAN-2003 (first entry)  
 XX  
 DE Anti-idiotypic VH sequence mimicking IgE conformational epitope.  
 XX  
 KW Human; IgE; immunoglobulin; antibody; epitope; mimotope;  
 KW lactic acid bacterium; allergy; vaccine; anti-allergic;  
 KW dermatological; anti-inflammatory; anti-idiotype.  
 XX  
 OS Homo sapiens.  
 XX  
 FT EPI239032-A1.  
 FT  
 XX 11-SEP-2002.  
 XX  
 XX 02-MAR-2001; 2001EP-0105138.  
 XX  
 XX 02-MAR-2001; 2001EP-0105138.  
 XX  
 XX (NEST ) SOC PROD NESTLE SA.  
 PA  
 XX Stadler BM, Vogel M, Germond J, Fritsche R;  
 XX  
 DR WPI; 2002-684058/74.  
 DR  
 XX  
 XX New bacterial strain of lactic acid bacterium group, expressing surface  
 PT polypeptide which contains peptide sequence mimicking at least part of  
 PT conformational epitope of immunoglobulin E, useful for treating allergy  
 PT  
 XX  
 XX Claim 4; Page 5; 19pp; English.  
 XX  
 XX The present invention relates to recombinant strains of lactic  
 CC acid bacteria that express surface polypeptides containing  
 CC peptides (mimotopes) or antibody fragments which mimic at least  
 CC part of a conformational epitope of an IgE molecule. These are  
 CC used in food and pharmaceutical compositions, in particular  
 CC vaccines, for the treatment or prevention of an allergic reaction  
 CC involving IgE, such as rhinitis, atopic dermatitis and erythema.  
 CC The mimotope peptides or antibody fragments are obtained by  
 CC screening random peptide and human Fab antibody phage display  
 CC libraries with an antibody directed to the Fc part of IgE. The  
 CC present sequence is the protein sequence of an anti-idiotypic Fab  
 CC heavy chain variable region (VH) sequence mimicking an IgE  
 CC conformational epitope.  
 CC  
 XX  
 SQ Sequence 126 AA;  
 Query Match 82.6%; Score 507; DB 23; Length 126;  
 Best Local Similarity 80.3%; Pred. No. 3.9e-36;  
 Matches 98; Conservative 6; Mismatches 10; Indels 8; Gaps 1;  
 QY 1 LESGGLVKSPTSLTCTVSGGSIIRSGYMSWIRPPGKLEWIGIYHSGNTYNNPS 60  
 DB 5 LESGGLVKSPTSLTCTVSGGSIIRSGYMSWIRPPGKLEWIGIYHSGNTYNNPS 64  
 QY 61 LKSRVTMSVDTSKNFSRLTSSVTAADTAAYVYCARSDG-----YTLDNMGCGTLVTV 112  
 DB 65 LKSRVTMSVDTSKNFSRLTSSVTAADTAAYVYCARSDG-----YTLDNMGCGTLVTV 124  
 QY 113 SS 114  
 DB 125 SS 126  
 RESULT 14  
 ID ABG80712 standard; Peptide: 251 AA.

XX AC ABG80712;  
 XX DT 29-NOV-2002 (first entry)  
 XX DE Amyloid peptide containing an attachment site #2.  
 XX MM Molecular antigen array; Vaccine; antigen; antimicrobial; mutant;  
 XX molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutein;  
 XX graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;  
 XX adult respiratory distress syndrome; ARDS; Crohn's disease;  
 XX allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 XX Grave's disease; systemic lupus erythematosus; osteoporosis;  
 XX inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
 XX immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
 XX angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
 XX rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 XX enterokinase; cysteine-containing linker.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN MO200256907-A2.  
 XX PD 25-JUL-2002.  
 XX PF 21-JAN-2002; 2002MO-IB00168.  
 XX PR 19-JAN-2001; 2001US-262379P.  
 XX PR 04-MAY-2001; 2001US-288549P.  
 XX PR 05-OCT-2001; 2001US-326989P.  
 XX PR 07-NOV-2001; 2001US-331045P.  
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 XX PA (NOVS) NOVARTIS PHARMA AG.  
 XX PA (MAUR/) MAURER P.  
 XX PA (LECH/) LECHNER F.  
 XX PA (ORTM/) ORTMANN R.  
 XX PA (LUEO/) LUEBEND R.  
 XX PA (STAU/) STAUFENBIEL M.  
 XX PA (FREY/) FREY P.  
 XX PI Maurer P., Lechner F., Ortman R., Luegend R., Staufenbiel M., Frey P;  
 XX PI Renner WA, Bachmann M., Tissot A., Seibel P., Plosek C;  
 XX DR WPI; 2002-636514/68.  
 XX PT Molecular antigen array used in the production of vaccines for  
 XX PT infectious diseases -  
 XX PS Claim 38; Page 227; 418bp; English.  
 XX CC The invention relates to a composition comprising: (a) a non-natural  
 XX CC molecular scaffold comprising: (i) a core particle selected from:  
 XX CC (1) a core particle of a non-natural origin; and (2) a core particle of  
 XX CC natural origin; and (ii) an organism comprising at least one first  
 XX CC attachment site, where the organism is connected to the core particle by  
 XX CC at least one covalent bond; (b) an antigen or antigenic determinant with  
 XX CC at least one second attachment site, where the antigen or antigenic  
 XX CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and  
 XX CC where the second attachment site is selected from: (i) an attachment site  
 XX CC not naturally occurring with the antigen or antigenic determinant; and  
 XX CC (ii) an attachment site naturally occurring with the antigen or  
 XX CC antigenic determinant, where the second attachment site is capable of  
 XX CC association through at least one non-peptide bond to the first attachment  
 XX CC site; and where the antigen or antigenic determinant and the scaffold  
 XX CC interact through the association to form an ordered and repetitive  
 XX CC antigen array. Also included is a process for producing a non-naturally  
 XX CC occurring ordered and repetitive antigen array. The composition is used  
 XX CC in immunisation and as a vaccine for diseases such as influenza,  
 XX CC graft versus host disease, IGE-mediated allergic reactions, anaphylaxis,  
 XX CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic  
 XX CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's

CC disease, systemic lupus erythematosus, inflammatory immune diseases,  
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's  
 CC disease, osteoporosis and infectious diseases. The present sequence is  
 CC a modified antigen for use in the array of the invention. The antigen is  
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a  
 CC cysteine-containing N- or C-terminal linker peptide which serves as the  
 CC attachment point to a virus like particle or bacterial protein (the  
 CC scaffold protein).  
 XX SQ Sequence 251 AA;  
 XX QY Query Match 82.6%; Score 507; DB 23; Length 251;  
 XX QY Best Local Similarity 80.3%; Pred. No. 86-36; Indels 8; Gaps 1;  
 XX QY Matches 98; Conservative 6; Mismatches 10;  
 XX DB 1 LESGPQLVXPSQTLTLCTVSGSIRSGGYWSMIRPPGKLEWIGYIYHSGNTYNS 60  
 XX DB 20 LESGPQLVXPSFTLSLCTVSGSISGGYWTWIRPPGKLEWIGYIYHSGNTYNS 79  
 XX DB 61 LKSRVTMSVDTSKNHFSLRLSSVTADPAVYVCARSDG-----YTLDMNGCGTIVTV 112  
 XX DB 80 LKSRVTMSVDTSKNHFSLRLSSVTADPAVYVCAREBETGLYPPYIYDVGITIVTV 139  
 XX QY 113 SS 114  
 XX DB 140 SS 141  
 XX DB  
 XX RESULT 15  
 XX ABP45983  
 XX ID ABP45983 standard; Protein; 252 AA.  
 XX AC ABP45983;  
 XX DT 19-AUG-2002 (first entry)  
 XX DE Human Blys binding scFv SEQ ID 1994.  
 XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostratic;  
 XX KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 XX KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 XX KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX OS Homo sapiens.  
 XX OS MO200202641-A1.  
 XX PN 10-JAN-2002.  
 XX PD 15-JUN-2001; 2001WO-US19110.  
 XX PF 16-JUN-2000; 2000US-212210P.  
 XX PR 17-OCT-2000; 2000US-240816P.  
 XX PR 16-MAR-2001; 2001US-276248P.  
 XX PR 21-MAR-2001; 2001US-277379P.  
 XX PR 25-MAY-2001; 2001US-293499P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX DR WPI; 2002-114799/15.  
 XX PT Antidodies against B lymphocyte stimulating polypeptides, useful for  
 XX PT the diagnosis and treatment of cancers and immune disorders -  
 XX PS Claim 1; Page 2779-2780; 3148bp; English.  
 XX

|                       |                 |                  |           |             |
|-----------------------|-----------------|------------------|-----------|-------------|
| Query Match           | 82.6%           | Score 507;       | DB 23;    | Length 252; |
| Best Local Similarity | 81.5%;          | Pred. No. 8e-36; |           |             |
| Matches 97;           | Conservative 6; | Mismatches 10;   | Indels 6; | Gaps 1;     |

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Db            6    ESGGGLVMPSCQTLLSLTCTVASCGRISSDDIYWMSNIROHPGGLELMIGVIHSGSTYYNPETL 65

**QY**            62   KSRVTMSVDTSKNNHFSLRLSSVTADPAAYVYCQR-----SDGYITLDNMCGGTLYTVSS 114

**Db**            66   KSRYVMSVDTSKNQYSLSLTASSVTADPAAYVICALRPDADYGDYGEPYMQGMATVVS 124

Search completed: February 10, 2004, 18:36:10  
Job time : 35.3727 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:39:30 ; Search time 26.2545 Seconds  
(without alignments)  
909.160 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614  
Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDMGQGLTVTVSS 114

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 614   | 100.0       | 114    | 15    | US-10-027-725A-9  |
| 2          | 600   | 97.7        | 114    | 15    | US-10-027-725A-8  |
| 3          | 556   | 90.6        | 114    | 15    | US-10-027-725A-7  |
| 4          | 524.5 | 85.4        | 121    | 12    | US-10-309-762-152 |
| 5          | 524   | 85.3        | 118    | 12    | US-10-309-762-138 |
| 6          | 523.5 | 85.3        | 123    | 12    | US-10-309-762-10  |
| 7          | 521   | 84.9        | 120    | 12    | US-10-309-762-13  |
| 8          | 521   | 84.9        | 120    | 12    | US-10-309-762-144 |
| 9          | 521   | 84.9        | 122    | 12    | US-10-309-762-147 |
| 10         | 520   | 84.7        | 221    | 11    | US-09-972-656-80  |
| 11         | 519.5 | 84.6        | 121    | 12    | US-10-309-762-151 |
| 12         | 519.5 | 84.6        | 125    | 12    | US-10-309-762-11  |
| 13         | 517.5 | 84.3        | 119    | 12    | US-10-309-762-140 |
| 14         | 516.5 | 84.1        | 123    | 12    | US-10-309-762-12  |
| 15         | 516   | 84.0        | 124    | 12    | US-10-309-762-75  |

|    |       |      |     |    |                    |                   |
|----|-------|------|-----|----|--------------------|-------------------|
| 16 | 516   | 84.0 | 143 | 12 | US-10-309-762-96   | Sequence 96, Appl |
| 17 | 515.5 | 84.0 | 117 | 12 | US-10-330-613-13   | Sequence 13, Appl |
| 18 | 515.5 | 84.0 | 117 | 12 | US-10-330-530-13   | Sequence 13, Appl |
| 19 | 514   | 83.7 | 120 | 12 | US-10-309-762-128  | Sequence 128, App |
| 20 | 514   | 83.7 | 120 | 12 | US-10-309-762-139  | Sequence 139, App |
| 21 | 514   | 83.7 | 121 | 12 | US-10-308-817-137  | Sequence 137, App |
| 22 | 513   | 83.6 | 116 | 12 | US-10-309-762-127  | Sequence 127, App |
| 23 | 512.5 | 83.5 | 125 | 12 | US-10-309-762-8    | Sequence 8, Appl  |
| 24 | 512.5 | 83.5 | 125 | 12 | US-10-309-762-16   | Sequence 16, Appl |
| 25 | 511.5 | 83.3 | 119 | 12 | US-10-309-762-131  | Sequence 131, App |
| 26 | 511   | 83.2 | 110 | 12 | US-10-309-762-74   | Sequence 74, Appl |
| 27 | 510.5 | 83.1 | 123 | 12 | US-10-309-762-9    | Sequence 9, Appl  |
| 28 | 510.5 | 83.1 | 127 | 12 | US-10-309-762-14   | Sequence 14, Appl |
| 29 | 508.5 | 82.8 | 125 | 12 | US-10-309-762-153  | Sequence 153, App |
| 30 | 508   | 82.7 | 172 | 15 | US-10-153-182-21   | Sequence 21, Appl |
| 31 | 507.5 | 82.7 | 117 | 12 | US-10-330-613-5    | Sequence 5, Appl  |
| 32 | 507.5 | 82.7 | 117 | 12 | US-10-330-530-5    | Sequence 5, Appl  |
| 33 | 507.5 | 82.7 | 123 | 12 | US-10-309-762-17   | Sequence 17, Appl |
| 34 | 507   | 82.6 | 126 | 10 | US-09-974-449-6    | Sequence 6, Appl  |
| 35 | 507   | 82.6 | 252 | 11 | US-09-880-748-1994 | Sequence 1994, Ap |
| 36 | 506.5 | 82.5 | 251 | 12 | US-10-309-762-143  | Sequence 143, App |
| 37 | 506.5 | 82.5 | 251 | 12 | US-10-120-414-75   | Sequence 75, Appl |
| 38 | 506.5 | 82.5 | 253 | 11 | US-09-880-748-1619 | Sequence 1619, Ap |
| 39 | 505.5 | 82.3 | 123 | 12 | US-10-309-762-18   | Sequence 18, Appl |
| 40 | 505.5 | 82.3 | 123 | 12 | US-10-309-762-19   | Sequence 19, Appl |
| 41 | 503   | 81.9 | 252 | 11 | US-09-880-748-1329 | Sequence 1329, Ap |
| 42 | 502.5 | 81.8 | 119 | 14 | US-10-025-687-5    | Sequence 5, Appl  |
| 43 | 502.5 | 81.8 | 119 | 15 | US-10-125-687-5    | Sequence 5, Appl  |
| 44 | 502   | 81.8 | 118 | 12 | US-10-078-7578-52  | Sequence 52, Appl |
| 45 | 501   | 81.6 | 256 | 11 | US-09-880-748-1607 | Sequence 1607, Ap |

#### ALIGNMENTS

RESULT 1  
US-10-027-725A-9  
; Sequence 9, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof  
; FILE REFERENCE: 25401.4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-9

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Best Local Similarity 100.0%; Pred. No. 4.6e-45;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 LESGPGLVKPSQTLSTCTVSGGSIRSGGYWSWIRPGKLEWIGIYHSGNTYVPS 60  
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; Sequence 8, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:

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; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8

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Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRQPEKGLWIGYIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match          90.6%; Score 556; DB 15; Length 114;
Best Local Similarity 90.4%; Pred. No. 9.6e-44;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRQPEKGLWIGYIYHSGNTYNNPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRQPEKGLWIGYIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
```

```
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152

Query Match          85.4%; Score 524.5; DB 12; Length 121;
Best Local Similarity 86.2%; Pred. No. 8e-41;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRQPEKGLWIGYIYHSGNTYNNPSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRQPEKGLWIGYIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 118

RESULT 5
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138

Query Match          85.3%; Score 524; DB 12; Length 118;
Best Local Similarity 88.5%; Pred. No. 8.6e-41;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRQPEKGLWIGYIYHSGNTYNNPSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRQPEKGLWIGYIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 118

RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
```



FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-10

Query Match 85.3%; Score 523.5; DB 12; Length 123;  
Best Local Similarity 85.6%; Pred. No. 1e-40; Indels 5; Gaps 1;  
Matches 101; Conservative 5; Mismatches 7;

OY 2 ESGPLVPSQTLSTCTVSGGSIRSGYMSWIRPQKGLWIGIYHSGNTYYNPSL 61  
DB 6 ESGPLVPSQTLSTCTVSGGSISGGYMSWIRQHGKGLWIGIYHSGNTYYNPSL 65  
OY 62 KSRVTMSYDTSKNHPSLRSLSSVTADTAIVYVCARS-----DGYLDNMGGTLVTSS 114  
DB 66 KSRVTISYDTSKNQPSLKLSSVTADTAIVYVCARAGKYSGSYDYGQGTLLVTSS 123

RESULT 7  
US-10-309-762-13  
Sequence 13, Application US/10309762  
Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudae, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-13

Query Match 84.9%; Score 521; DB 12; Length 120;  
Best Local Similarity 87.1%; Pred. No. 1.7e-40; Indels 4; Gaps 2;  
Matches 101; Conservative 5; Mismatches 6;

OY 2 ESGPLVPSQTLSTCTVSGGSIRSGYMSWIRPQKGLWIGIYHSGNTYYNPSL 61  
DB 6 ESGPLVPSQTLSTCTVSGGSISGGYMSWIRQHGKGLWIGIYHSGNTYYNPSL 65  
OY 62 KSRVTMSYDTSKNHPSLRSLSSVTADTAIVYVCARS---LDNMGGTLVTSS 114  
DB 66 KSRVTISYDTSKNQPSLKLSSVTADTAIVYCAR-DGNYVWFYDLMGRTLLVTSS 120

RESULT 8  
US-10-309-762-14  
Sequence 14, Application US/10309762  
Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudae, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 144  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-144

Query Match 84.9%; Score 521; DB 12; Length 120;  
Best Local Similarity 87.1%; Pred. No. 1.7e-40; Indels 4; Gaps 2;  
Matches 101; Conservative 5; Mismatches 6;

OY 2 ESGPLVPSQTLSTCTVSGGSIRSGYMSWIRPQKGLWIGIYHSGNTYYNPSL 61  
DB 6 ESGPLVPSQTLSTCTVSGGSISGGYMSWIRQHGKGLWIGIYHSGNTYYNPSL 65  
OY 62 KSRVTMSYDTSKNHPSLRSLSSVTADTAIVYVCARS---LDNMGGTLVTSS 114  
DB 66 KSRVTISYDTSKNQPSLKLSSVTADTAIVYCAR-DGNYVWFYDLMGRTLLVTSS 120

RESULT 9  
US-10-309-762-147  
Sequence 147, Application US/10309762  
Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudae, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 147  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-147

Query Match 84.9%; Score 521; DB 12; Length 122;  
Best Local Similarity 85.5%; Pred. No. 1.7e-40; Indels 8; Gaps 1;  
Matches 100; Conservative 5; Mismatches 8;

OY 2 ESGPLVPSQTLSTCTVSGGSIRSGYMSWIRPQKGLWIGIYHSGNTYYNPSL 61  
DB 6 ESGPLVPSQTLSTCTVSGGSISGGYMSWIRQHGKGLWIGIYHSGNTYYNPSL 65  
OY 62 KSRVTMSYDTSKNHPSLRSLSSVTADTAIVYCAR-----SDGYLDNMGGTLVTSS 114  
DB 66 KSRVTISYDTSKNQPSLKLSSVTADTAIVYCARIYDILDTGMDVGGTTLVTSS 122

RESULT 10  
US-09-972-656-80  
Sequence 80, Application US/09972656  
Publication No. US20030099647A1  
GENERAL INFORMATION:  
APPLICANT: Deshpande, Rajendra  
APPLICANT: Tsai, Mei-Mei  
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
TITLE OF INVENTION: Neutralizing Activity

```
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972.656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 80
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-656-80
```

```
Query Match      84.7%; Score 520; DB 11; Length 221;
Best Local Similarity 86.7%; Pred. No. 3.8e-40;
Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 2 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRQPKGLEWIGYIYHSGNTYNNPSL 61
    |||||
DB 6 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRQPKGLEWIGYIYHSGNTYNNPSL 65
    |||||
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSGQGTLDNMGCGTLVTYSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARSGQGTLDNMGCGTLVTYSS 118
```

```
RESULT 11
US-10-309-762-151
Sequence 151, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Hands, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 151
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-151
```

```
Query Match      84.6%; Score 519.5; DB 12; Length 121;
Best Local Similarity 86.2%; Pred. No. 2.3e-40;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
```

```
QY 2 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRQPKGLEWIGYIYHSGNTYNNPSL 61
    |||||
DB 6 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRQPKGLEWIGYIYHSGNTYNNPSL 65
    |||||
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSD--DGYTLDNMGCGTLVTYSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARVLLMFQGYGMDVWGQGTITVTYSS 121
```

```
RESULT 12
US-10-309-762-11
Sequence 11, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Hands, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
```

```
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-11
```

```
Query Match      84.6%; Score 519.5; DB 12; Length 125;
Best Local Similarity 83.3%; Pred. No. 2.4e-40;
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;
```

```
QY 2 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRQPKGLEWIGYIYHSGNTYNNPSL 61
    |||||
DB 6 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRQPKGLEWIGYIYHSGNTYNNPSL 65
    |||||
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSD--DGY--TLDNMGCGTLVTYSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARITYPFLTGPDAFDIMGQGTIVTYSS 125
```

```
RESULT 13
US-10-309-762-140
Sequence 140, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Hands, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 140
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-140
```

```
Query Match      84.3%; Score 517.5; DB 12; Length 119;
Best Local Similarity 86.8%; Pred. No. 3.4e-40;
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
```

```
QY 2 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRQPKGLEWIGYIYHSGNTYNNPSL 61
    |||||
DB 6 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRQPKGLEWIGYIYHSGNTYNNPSL 65
    |||||
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSD--GYTLDNMGCGTLVTYSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARGYGMDVWGQGTITVTYSS 119
```

```
RESULT 14
US-10-309-762-12
Sequence 12, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Hands, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
```

```
FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-12

Query Match      84.1%; Score 516.5; DB 12; Length 123;
Best Local Similarity 83.9%; Pred. No. 4,4e-40;
Matches 99; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

Oy      2  ESGPGLVPSQTLSLTCTVSGSGSIRSGGYWMSWIRQPPKGLWIGYTHSGNTYYNPSL 61
        |||
Db      6  ESGPGLVPSQTLSLTCTVSGSGSIRSGGYWMSWIRQHPKGLWIGYTHSGNTYYNPSL 65
        |||

Oy      62 KSRVTMSYDTSKNHPSLRSLSSVTADTAIVYYCAR-----SDGYTLDNWGQGLTVTVSS 114
        |||
Db      66 KSRVTISYDTSKNQPSLRSLSSVTADTAIVYYCARVTLWFGEDYGYDVWGQGLTVTVSS 123
        |||

RESULT 15
US-10-309-762-75
; Sequence 75, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Guddae, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 75
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-75

Query Match      84.0%; Score 516; DB 12; Length 124;
Best Local Similarity 84.0%; Pred. No. 4,9e-40;
Matches 100; Conservative 6; Mismatches 7; Indels 6; Gaps 2;

Oy      2  ESGPGLVPSQTLSLTCTVSGSGSIRSGGYWMSWIRQPPKGLWIGYTHSGNTYYNPSL 61
        |||
Db      6  ESGPGLVPSQTLSLTCTVSGSGSIRSGGYWMSWIRQHPKGLWIGYTHSGNTYYNPSL 65
        |||

Oy      62 KSRVTMSYDTSKNHPSLRSLSSVTADTAIVYYCARSD-----GYT-LDNWGQGLTVTVSS 114
        |||
Db      66 KSRVTISYDTSKNQPSLRSLSSVTADTAIVYYCARVTLWFGEDYGYDVWGQGLTVTVSS 124
        |||

Search completed: February 10, 2004, 19:03:03
Job time : 27.2545 secs
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 : Search time 11.7455 Seconds  
(without alignments)  
410.664 Million cell updates/sec

Title: US-10-027-725A-9  
Perfect score: 614  
Sequence: 1 LESRGLVKSQTLSINCTV.....RSDGTYLDNMGQGLVTVSS 114

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                 | Description        |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1          | 521   | 84.9        | 473    | US-09-049-672A-4   | Sequence 4, Appl   |
| 2          | 502.5 | 81.8        | 119    | US-09-025-769B-39  | Sequence 39, Appl  |
| 3          | 502.5 | 81.8        | 119    | US-09-025-769B-65  | Sequence 65, Appl  |
| 4          | 496   | 80.8        | 122    | US-08-360-125-11   | Sequence 11, Appl  |
| 5          | 496   | 80.8        | 122    | US-08-450-578-11   | Sequence 11, Appl  |
| 6          | 496   | 80.8        | 122    | US-09-017-628-11   | Sequence 11, Appl  |
| 7          | 496   | 80.8        | 122    | US-09-014-880-11   | Sequence 11, Appl  |
| 8          | 496   | 80.8        | 122    | US-08-450-363-11   | Sequence 11, Appl  |
| 9          | 491   | 80.0        | 118    | US-09-025-769B-25  | Sequence 25, Appl  |
| 10         | 487.5 | 79.4        | 119    | US-08-360-125-5    | Sequence 5, Appl   |
| 11         | 487.5 | 79.4        | 119    | US-08-450-578-5    | Sequence 5, Appl   |
| 12         | 487.5 | 79.4        | 119    | US-09-017-628-5    | Sequence 5, Appl   |
| 13         | 487.5 | 79.4        | 119    | US-09-014-880-5    | Sequence 5, Appl   |
| 14         | 487.5 | 79.4        | 119    | US-08-450-363-5    | Sequence 5, Appl   |
| 15         | 472   | 76.9        | 244    | US-08-918-148-79   | Sequence 79, Appl  |
| 16         | 467   | 76.1        | 118    | US-08-545-809A-116 | Sequence 116, Appl |
| 17         | 466.5 | 76.0        | 142    | US-08-480-774A-2   | Sequence 2, Appl   |
| 18         | 463.5 | 75.5        | 250    | US-10-039-785-50   | Sequence 50, Appl  |
| 19         | 460.5 | 75.0        | 119    | US-08-652-816A-10  | Sequence 10, Appl  |
| 20         | 460   | 74.9        | 278    | US-09-260-527-3    | Sequence 3, Appl   |
| 21         | 457   | 74.4        | 118    | US-08-545-809A-142 | Sequence 142, Appl |
| 22         | 457   | 74.4        | 118    | US-09-343-698-6    | Sequence 6, Appl   |
| 23         | 450.5 | 73.4        | 219    | US-09-460-384-37   | Sequence 37, Appl  |
| 24         | 450   | 73.3        | 832    | US-08-630-820-7    | Sequence 37, Appl  |
| 25         | 449   | 73.1        | 126    | US-08-276-852-142  | Sequence 142, Appl |
| 26         | 449   | 73.1        | 126    | US-08-899-575-142  | Sequence 142, Appl |
| 27         | 449   | 73.1        | 126    | US-08-899-575-142  | Sequence 142, Appl |

|    |       |      |     |   |                    |                   |
|----|-------|------|-----|---|--------------------|-------------------|
| 28 | 449   | 73.1 | 126 | 5 | PCT-US95-08743-142 | Sequence 142, App |
| 29 | 448   | 73.0 | 118 | 3 | US-08-545-809A-123 | Sequence 123, App |
| 30 | 446.5 | 72.7 | 98  | 1 | US-08-478-039-75   | Sequence 75, Appl |
| 31 | 446.5 | 72.7 | 98  | 1 | US-08-478-349A-75  | Sequence 75, Appl |
| 32 | 446.5 | 72.7 | 123 | 2 | US-08-137-117D-64  | Sequence 64, Appl |
| 33 | 446.5 | 72.7 | 123 | 2 | US-08-436-717-64   | Sequence 64, Appl |
| 34 | 446.5 | 72.7 | 123 | 4 | US-08-793-450-4    | Sequence 4, Appl  |
| 35 | 446.5 | 72.7 | 138 | 1 | US-08-137-117D-69  | Sequence 69, Appl |
| 36 | 446.5 | 72.7 | 138 | 2 | US-08-436-717-69   | Sequence 69, Appl |
| 37 | 446.5 | 72.7 | 472 | 4 | US-08-793-450-8    | Sequence 8, Appl  |
| 38 | 444   | 72.3 | 150 | 4 | US-09-582-337-14   | Sequence 14, Appl |
| 39 | 442.5 | 72.1 | 124 | 1 | US-08-478-039-78   | Sequence 78, Appl |
| 40 | 442.5 | 72.1 | 124 | 1 | US-08-478-349A-78  | Sequence 78, Appl |
| 41 | 440   | 71.7 | 116 | 3 | US-08-545-809A-140 | Sequence 140, App |
| 42 | 439.5 | 71.6 | 476 | 3 | US-08-487-550-12   | Sequence 12, Appl |
| 43 | 439.5 | 71.6 | 476 | 4 | US-09-526-028-12   | Sequence 12, Appl |
| 44 | 439   | 71.5 | 244 | 4 | US-10-039-785-44   | Sequence 44, Appl |
| 45 | 435   | 70.8 | 120 | 4 | US-08-057-430A-26  | Sequence 26, Appl |

## ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
Sequence 4, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Yang, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049, 672A  
FILING DATE: HERewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANCUTU01

CLONE: 1513264  
US-09-049-672A-4

Query Match 84.9%; Score 521; DB 3; Length 473;  
Best Local Similarity 83.2%; Pred. No. 1.3e-44;  
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 2 EESGPGVLRKRSQTLSTLCYVSGSIRSGYVSWIRPPGKGLWIGIYHSNTYNNPSL 61  
DB 25 EESGPGVLRKRSQTLSTLCYVSGSIRSGYVSWIRPPGKGLWIGIYHSNTYNNPSL 84  
QY 62 KSRVTMSVDTSKNHSRLRSSTVTAADTAVYYCARSD-----GYTLDMNGQGLTVTVSS 114  
DB 85 KSRVTISVDTSKNHSRLRSSTVTAADTAVYYCARSDVGLRGVGMGDMWGQGLTVTVSS 143

RESULT 2  
US-09-025-769B-39  
Sequence 39, Application US/09025769B

GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 81.8%; Score 502.5; DB 4; Length 119;  
Best Local Similarity 85.3%; Pred. No. 1.8e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 EESGPGVLRKRSQTLSTLCYVSGSIRSGYVSWIRPPGKGLWIGIYHSNTYNNPSL 61  
DB 6 EESGPGVLRKRSQTLSTLCYVSGSIRSGYVSWIRPPGKGLWIGIYHSNTYNNPSL 63  
QY 62 KSRVTMSVDTSKNHSRLRSSTVTAADTAVYYCAR--SDG-YTLDMNGQGLTVTVSS 114  
DB 85 KSRVTISVDTSKNHSRLRSSTVTAADTAVYYCAR--SDG-YTLDMNGQGLTVTVSS 143

DB 64 KSRVTISVDTSKNHSRLRSSTVTAADTAVYYCARWGDGFYAMDYGGQGLTVTVSS 119

RESULT 3  
US-09-025-769B-65  
Sequence 65, Application US/09025769B  
Patent No. 6300064

GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-65

Query Match 81.8%; Score 502.5; DB 4; Length 119;  
Best Local Similarity 85.3%; Pred. No. 1.8e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 EESGPGVLRKRSQTLSTLCYVSGSIRSGYVSWIRPPGKGLWIGIYHSNTYNNPSL 61  
DB 6 EESGPGVLRKRSQTLSTLCYVSGSIRSGYVSWIRPPGKGLWIGIYHSNTYNNPSL 63  
QY 62 KSRVTMSVDTSKNHSRLRSSTVTAADTAVYYCAR--SDG-YTLDMNGQGLTVTVSS 114  
DB 64 KSRVTISVDTSKNHSRLRSSTVTAADTAVYYCARWGDGFYAMDYGGQGLTVTVSS 119

RESULT 4  
US-08-360-125-11  
Sequence 11, Application US/08360125  
Patent No. 5767246

GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246hiko ITO  
APPLICANT: Kazuhiko NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:

FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-11  
Query Match 80.8%; Score 496; DB 1; Length 122;  
Best Local Similarity 81.2%; Pred. No. 8.3e-43;  
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;  
QY 2 ESGPGLVKKPSQTSLTCTVSGSGSRSGYKMSWIRORPGKLEWIGYIHSGNTYNPSTL 61  
DB 6 ESGPGLVKKPSQTSLTCTVSGSGSRSGYKMSWIRORPGKLEWIGYIHSGNTYNPSTL 65  
QY 62 KSRVTMSVDTSKMFSLRLSSVTADTAAYVYCCASD----GYTLDNNGQGLTVYSS 114  
DB 66 KSRVTISVDTSKMFSLRLSSVTADTAAYVYCCASDGGYTGNDVWGQGLTVYSS 122  
RESULT 5  
US-08-450-578-11  
Sequence 11, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845hiko ITO  
APPLICANT: Kazuhito NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:

ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-11

Query Match 80.8%; Score 496; DB 2; Length 122;  
Best Local Similarity 81.2%; Pred. No. 8.3e-43;  
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQSLTSLCTVSGGSIRSGGYWMIROPKGLGWIYHSNTYNPBL 61  
DB 6 ESGPGLVKSQSLTSLCTVSGGSIRSGGYWMIROPKGLGWIYHSNTYNPBL 65  
QY 62 KSRVTMSVDTSKNHSRLISVTAAADTAAYVYCARSD----GYLDNMGGCTLVTVSS 114  
DB 66 KSRVTISVDTSKNQSLSKLSVTAAADTAAYVYCARSGSYGGYGMVWGQSTVTVSS 122

RESULT 6  
US-09-017-628-11  
Sequence 11, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287/hiko  
APPLICANT: NAGAIKE, Kazuhito  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02  
EARLIER FILING DATE: 1994-12-20  
EARLIER APPLICATION NUMBER: 08/360,135  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1

US-09-017-628-11

Query Match 80.8%; Score 496; DB 2; Length 122;  
Best Local Similarity 81.2%; Pred. No. 8.3e-43;  
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQSLTSLCTVSGGSIRSGGYWMIROPKGLGWIYHSNTYNPBL 61  
DB 6 ESGPGLVKSQSLTSLCTVSGGSIRSGGYWMIROPKGLGWIYHSNTYNPBL 65  
QY 62 KSRVTMSVDTSKNHSRLISVTAAADTAAYVYCARSD----GYLDNMGGCTLVTVSS 114  
DB 66 KSRVTISVDTSKNQSLSKLSVTAAADTAAYVYCARSGSYGGYGMVWGQSTVTVSS 122

RESULT 7  
US-09-014-880-11  
Sequence 11, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
US-09-014-880-11  
Query Match 80.8%; Score 496; DB 2; Length 122;  
Best Local Similarity 81.2%; Pred. No. 8.3e-43;  
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;  
QY 2 ESGPGLVKSQSLTSLCTVSGGSIRSGGYWMIROPKGLGWIYHSNTYNPBL 61



Db 6 ESGPLVPSRSTLSITCTVSGGSISSSYWGMIRQPPGKLEWIGSIYSGSTYVPSL 65  
Qy 62 KSRVTMSVDTSKNHSRLSSVTADTVAVYICARSD---GYTLDNWGQGLTVYSS 114  
66 KSRVTISVDTSKNPSLKLSSVTADTVAVYICARSGYGGYGMVWVGQGLTVYSS 122

## RESULT 8

US-08-450-363-11  
Sequence 11, Application US/08450363  
Patent No. 6436434  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiki TAGAWA  
APPLICANT: YOKO HIRAKAWA  
APPLICANT: No. 6436434Ihiko ITO  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C. U.S.A.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,363  
FILING DATE: May 25, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: protein  
TOPOLOGY: linear  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
ORGANELLE:  
IMMEDIATE SOURCE:

LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-11

Query Match 80.8% Score 496; DB 4; Length 122;  
Best Local Similarity 81.2% Pred. No. 8.3e-43;  
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

Qy 2 ESGPLVPSRSTLSITCTVSGGSISSSYWGMIRQPPGKLEWIGSIYSGSTYVPSL 61  
Db 6 ESGPLVPSRSTLSITCTVSGGSISSSYWGMIRQPPGKLEWIGSIYSGSTYVPSL 65  
Qy 62 KSRVTMSVDTSKNHSRLSSVTADTVAVYICARSD---GYTLDNWGQGLTVYSS 114  
Db 66 KSRVTISVDTSKNPSLKLSSVTADTVAVYICARSGYGGYGMVWVGQGLTVYSS 122

## RESULT 9

US-09-025-769B-25  
Sequence 25, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knapik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilaq, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-25

Query Match 80.0%; Score 491; DB 4; Length 118;  
Best local Similarity 84.3%; Pred. No. 2,5e-42;  
Matches 97; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRPPGKLEWIGIYHSGNTYNSPL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRPPGKLEWIGIYHSGNTYNSPL 63  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCA--RSDGTTLDNMGQGLTVTVSS 114  
DB 64 KSRVTISVDTSKNHFSLRLSSVTAADTAVYYCARGGGGGVFDYWGQGLTVTVSS 118

## RESULT 10

US-08-360-125-5  
Sequence 5, Application US/08360125  
Patent No. 5767246

GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246hiko ITO  
APPLICANT: Kazuhiko NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoch, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-360-125-5

Query Match 79.4%; Score 487.5; DB 1; Length 119;  
Best local Similarity 81.6%; Pred. No. 5,8e-42;  
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRPPGKLEWIGIYHSGNTYNSPL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYWSMIRPPGKLEWIGIYHSGNTYNSPL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-LDNMGQGLTVTVSS 114  
DB 66 KSRVTISVDTSKNHFSLRLSSVTAADTAVYYCARSTRRLGADYWGQGLTVTVSS 119

## RESULT 11

US-08-450-578-5  
Sequence 5, Application US/08450578  
Patent No. 5837845

GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845hiko ITO  
APPLICANT: Kazuhiko NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoch, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington

STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE: antibody GAH  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-578-5

Query Match 79.4%; Score 487.5; DB 2; Length 119;  
Best Local Similarity 81.6%; Pred. No. 5,8e-42;  
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;  
QY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNSL 61  
DB 6 ESGPGLVPSQTLSTCTVSGSGSISCGFYNNWIRHPGKLEWIGYIYHSGNTYNSL 65  
QY 62 KSRVTMSVDTSKNPSRLSSVTADPAVYVCARSDGYT-LDNNQGGTLTVSS 114  
DB 66 KSRVTISLDTSKSPSLKSLSLTADPAVYVCARSTRLRGADYMGQGTMTVSS 119  
RESULT 12  
US-09-017-628-5  
Sequence 5, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287jhiko  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 5  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH  
US-09-017-628-5  
Query Match 79.4%; Score 487.5; DB 2; Length 119;  
Best Local Similarity 81.6%; Pred. No. 5,8e-42;  
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;  
QY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNSL 61  
DB 6 ESGPGLVPSQTLSTCTVSGSGSISCGFYNNWIRHPGKLEWIGYIYHSGNTYNSL 65  
QY 62 KSRVTMSVDTSKNPSRLSSVTADPAVYVCARSDGYT-LDNNQGGTLTVSS 114  
DB 66 KSRVTISLDTSKSPSLKSLSLTADPAVYVCARSTRLRGADYMGQGTMTVSS 119  
RESULT 13  
US-09-014-880-5  
Sequence 5, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
APPLICATION DATA: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
US-09-014-880-5

Query Match 79.4%; Score 487.5; DB 2; Length 119;  
Best Local Similarity 81.6%; Pred. No. 5.8e-42;  
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;  
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWMSIRPGKLEWIGYIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSISCGFYWNWIRHDPKGLWIGYIYSGSTYNNPSL 65  
QY 62 KSRVTSVDPKSKHFSRLSSVTAAADTAAYVYCARSDGYT-LDNWGQSTLVTVSS 114  
DB 66 KSRVTSVDPKSKHFSRLSSVTAAADTAAYVYCARSDGYT-LDNWGQSTLVTVSS 119

RESULT 14  
US-08-450-363-5  
Sequence 5, Application US/08450363  
Patent No. 6435434  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 6436434ihiko ITO  
APPLICANT: Kazuhito NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,363  
FILING DATE: May 25, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-5

Query Match 79.4%; Score 487.5; DB 4; Length 119;  
Best Local Similarity 81.6%; Pred. No. 5.8e-42;  
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;  
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWMSIRPGKLEWIGYIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSISCGFYWNWIRHDPKGLWIGYIYSGSTYNNPSL 65

```

QY      62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYYCARSDGYT-LDNMGQGLTVTSS 114
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66 KSRVTIISLPTSKSQFSLKLSSLTAAADTAIVYYCARSTRLRGADYWGQGTWTVSS 119

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RESULT 15  
TIS-08-918

US-08-918-148-79  
 : Sequence 79, Application US/08918148A  
 : Patent No. 6342820  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Adams, Camellia  
 : APPLICANT: W.  
 : APPLICANT: Carter, Paul J.  
 : APPLICANT: Fendly, Brian M.  
 : APPLICANT: Gurney, Austin L.  
 : TITLE OR INVENTION: Agonist Antibodies  
 : FILE REFERENCE: P0979  
 : CURRENT APPLICATION NUMBER: US/08/918.148A  
 : CURRENT FILING DATE: 1997-08-25  
 : NUMBER OF SEQ ID NOS: 79  
 : SEQ ID NO 79  
 : LENGTH: 244  
 : TYPE: PRT  
 : ORGANISM: artificial  
 : US-08-918-148-79

|                       |              |                    |               |             |
|-----------------------|--------------|--------------------|---------------|-------------|
| Query Match           | 76.9%;       | Score 472;         | DB 4;         | Length 244; |
| Best Local Similarity | 81.4%;       | Pred. No. 4.9e-40; |               |             |
| Matches 92;           | Conservative | 9;                 | Mismatches 8; | Indels 4;   |
|                       |              |                    |               | Gaps 2      |

Qy 2 ESAGGLVXPSQTLTILCTVSCGSLRSGGYWMSLRPGKGLMIGIYHSGMTYNNPSL 65  
Db 8 QSGGGLVXKPSSTLILCTVSCGSLSS--YMSWLRPGKGLMIGIYHSSGNTNNPSL 65  
Qy 62 KSRVTMSVDTSKMHFSLRLSSVTADPAVNYCARSDGYTLDNNGGGLTVTVSS 114  
Db 66 KSRVTISVDTSKQFSLKLSSTVADPAVNYCA--GRYPDWGRGTMVTVSS 116

Search completed: February 10, 2004, 18:42:07  
Job time : 12.7455 secs

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```

XX 11-JUL-2002.
PD
XX 27-DEC-2001; 2001WO-SE02908.
PF
XX 29-DEC-2000; 2000SE-0004892.
PR
XX (PHMA ) PHARMACIA DIAGNOSTICS AB.
PA
XX Flicker S, Steinberger P, Kraft D, Valenta R;
PI
XX WPI; 2002-583604/62.
DR
XX N-PSDB; ABRK9640.
XX
XX Group 2 allergen-specific immunoglobulin (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for
PT environmental allergen detection -
XX
XX Disclosure; Page 39; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's
CC IgE antibodies to Phl p 2 (a major timothy grass pollen allergen).
CC The group 2 allergen-specific Fabs of the invention may be useful for
CC environmental allergen detection and for standardisation of allergen
CC extracts. The Fabs - or a vaccine against a type I allergy is useful for
CC passive immunotherapy of type I allergy, it is also useful for
CC diagnosing a type I allergy. The allergen-specific Fabs of the invention
CC are useful for inter alia, diagnosis, therapy and prevention of type
CC I allergy. They are also useful for identification of group 2
CC allergen-containing pollen and may be used for blocking the binding of
CC grass pollen allergic patient's IgE antibodies to Phl p 2. The present
CC sequence represents the human IgG fab, clone 94 light chain protein of
CC the invention.
XX
XX Sequence 106 AA;
SQ
XX
XX Query Match 98.2%; Score 533; DB 23; Length 106;
XX Best Local Similarity 99.1%; Pred. No. 2.2e-33;
XX Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGRVTISCRASQRIINTYLMWYQHKPKAPKLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGRVTISCRASQRIINTYLMWYQHKPKAPKLIYAASSLSQGVPSRF 60
QY 61 SSGSGYGTDTFTLTISLQPEDFASYYCQESLSASVTFGGGTKEIKR 106
DB 61 SSGSGYGTDTFTLTISLQPEDFASYYCQESLSASVTFGGGTKEIKR 106

RESULT 2
AAR54260
ID AAR54260 standard; protein; 107 AA.
XX
XX AAR54260;
AC
XX
XX 25-MAR-2003 (updated)
DT 10-NOV-1994 (first entry)
XX
XX Anti-HIV gp120 immunoglobulin light chain variable region b22.
XX
XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
XX variable region; framework; complementarity determining region.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..21
FT Region /label= FRI
FT

```

```

FT Region 22..33
FT /label= CDR1
FT 34..48
FT /label= FR2
FT 49..55
FT /label= CDR2
FT 56..87
FT /label= FR3
FT 88..95
FT /label= CDR3
FT 96..107
FT /label= FR4
XX
XX WO9407922-A1.
XX
XX 14-APR-1994.
PD
XX
XX 30-SEP-1993; 93WO-US09328.
XX
XX 30-SEP-1992; 92US-0954148.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Barbas CF, Burton DR, Lerner RA;
PI
XX WPI; 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
XX
XX Claim 5; Page 189; 248pp; English.
XX
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the Mab regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence AAR54260 neutralises HIV1
CC gp120.
XX
XX (Updated on 25-MAR-2003 to correct FN field.)
SQ
XX
XX Sequence 107 AA;
XX
XX Query Match 87.5%; Score 475; DB 15; Length 107;
XX Best Local Similarity 87.7%; Pred. No. 5.4e-29;
XX Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGRVTISCRASQRIINTYLMWYQHKPKAPKLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGRVTITCRASQSISSYLMWYQHKPKAPKLIYAASSLSQGVPSRF 60
QY 61 SSGSGYGTDTFTLTISLQPEDFASYYCQESLSASVTFGGGTKEIKR 106
DB 61 SSGSGYGTDTFTLTISLQPEDFATYYCQGSYSPYTFGGGTKEIKR 106

RESULT 3
AAW01283
ID AAW01283 standard; Protein; 107 AA.
XX
XX AAW01283;
AC
XX
XX 29-JAN-1997 (first entry)
DT
XX
XX VL region of HIV neutralising Mab, clone b22 and B35.
XX
XX Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW Mab; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
XX virus infectivity assay; precursor gp160; immunocompetence; human;
XX anti-HIV antibody; detection; HIV infection.
XX

```



|          |   |  |               |
|----------|---|--|---------------|
| XX       |   | Homosapiens.                                       |               |
| OS       |   |  |               |
| XX       |   |  |               |
| FH       | Key   | Location/Qualifiers                                |               |
| FT       | Region  | /label= FR1  | 1..21         |
| FT       | Region  | /label= CDR1                                       | 22..32        |
| FT       | Region  | /label= FR2  | 33..47        |
| FT       | Region  | /label= FR2  | 48..54        |
| FT       | Region  | /label= CDR2                                       | 55..86        |
| FT       | Region  | /label= FR3  | 87..95        |
| FT       | Region  | /label= CDR3                                       | 96..107       |
| FT       | Region  | /label= FR4  |               |
| XX       |   |  |               |
| PN       |   | WO9602273-A1.                                      |               |
| XX       |   |  |               |
| PD       |   | 01-FEB-1996.                                       |               |
| PF       |   | 11-JUL-1995;                                       | 95WO-US08743. |
| PR       |   | 18-JUN-1994;                                       | 94US-0276852. |
| PA       | (SCRI )   | SCRIPPS RES INST.                                  |               |
| PI       | Barbas CF,  | Burton DR,   | Lerner RA;    |
| PI       | WPI;  | 1996-179601/18.                                    |               |
| PT       | Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in      |  |               |
| PT       | passive immuno:therapy and detection of HIV infection.                |  |               |
| XX       |   |  |               |
| PS       | Example; Fig 11; 366bp; English.                                      |  |               |
| CC       | The sequences given in AAW01261-92 represent the light chain variable |  |               |
| CC       | regions (VL) of a series of monoclonal antibodies (Mab's) which are   |  |               |
| CC       | immunoreactive with HIV glycoprotein gp120 and are capable of         |  |               |
| CC       | neutralising HIV. This sequence represents the sequence of the JK2    |  |               |
| CC       | gene clones, b22 and B35. A Mab containing this VL sequence has the   |  |               |
| CC       | capacity to reduce HIV infectivity titre in an in vivo virus          |  |               |
| CC       | infectivity assay by 50 % at a concentration of less than 700 ng      |  |               |
| CC       | of antibody/ml, and binds mature gp120 preferentially over the        |  |               |
| CC       | precursor gp160. The Mab may be used for determining immunocompetence |  |               |
| CC       | of a human anti-HIV antibody and in the detection of HIV infection.   |  |               |
| XX       |   |  |               |
| SQ       | Sequence  | 107 AA;  |               |
|          | Query Match   | 87.5%; Score 475; DB 17; Length 107;               |               |
|          | Best Local Similarity   | 87.7%; Pred. No. 5.4e-29;                          |               |
|          | Matches   | 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0 |               |
| Dy       | 1 ELTGSPLSLASVGDGVITISCRASGRINTYINMWYQHKGKAPKLLIYAASSIQGVPSPRF        | 60   |               |
| Dd       | 1 ELTGPSLSLASVGDGVITICRASGISISSYLNMWYQOKGKAPKLIIYAASSIQGVPSPRF        | 60   |               |
| Dy       | 61 SGSGGTDPFTLTISSLOFEDPASYYCOESLASSTFGCGTKVEIKR                      | 106  |               |
| Dd       | 61 SGSGGTDPFTLTISSLOFEDPATYVCOSYSTPYTFGGCTKLEIKR                      | 106  |               |
| RESULT 4 |   |  |               |
| ID       | AA95135   |  |               |
| XX       | AA95135 standard; Protein; 107 AA.                                    |  |               |
| AC       | AA95135;  |  |               |
| DT       | 30-JUN-2000 (first entry)   |  |               |
| DE       | Anti-gp120 antibody light chain variable region from clone b22.       |  |               |

|          |   |   |
|----------|---|---|
| XX       |   | Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise; |
| KW       |   | reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;  |
| XX       |   | glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.  |
| OS       | Homo sapiens.   |   |
| XX       |   |   |
| PN       | AU9948756-A.  |   |
| XX       |   |   |
| PD       | 17-FEB-2000.  |   |
| XX       |   |   |
| PF       | 16-SEP-1999;  | 99AU-0048756.   |
| XX       |   |   |
| PR       | 16-SEP-1999;  | 99AU-0048756.   |
| XX       |   |   |
| PA       | (SCRI ) SCRIPPS RES INST.   |   |
| PI       | Burton DR, Barbas CF, Lerner RA;  |   |
| DR       | WPI; 2000-293393/26.  |   |
| XX       |   |   |
| PT       | Novel human monoclonal antibodies which immunoreact with and neutralise   |   |
| PT       | human immunodeficiency virus useful for treating HIV infections           | -   |
| PS       |   |   |
| XX       | Example 9; Figure 11; 366pp; English.                                     |   |
| CC       | The present sequence represents a fragment of an anti-human               |   |
| CC       | immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  |   |
| CC       | a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV    |   |
| CC       | mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  |   |
| CC       | gp160 and neutralises HIV and which reduces HIV infectivity titre in an   |   |
| CC       | in vitro virus infectivity assay by 50%, at a concentration of less than  |   |
| CC       | 700 ng/ml. The antibodies are used as reagents for the diagnosis and      |   |
| CC       | immunotherapy of HIV induced disease. They are useful as neutralising     |   |
| CC       | field isolates and provide useful information regarding the               |   |
| CC       | immunocompetence of an immune response in HIV infected patients. The      |   |
| CC       | monoclonal antibodies are useful for producing anti-idiotypic antibodies  |   |
| CC       | which can be used to screen human monoclonal antibodies to identify       |   |
| CC       | whether the antibody has the same binding specificity as the antibodies   |   |
| CC       | of the invention. The neutralising antibodies define new epitopes on the  |   |
| CC       | HIV gp120 and gp41 glycoproteins, thus increasing the availability of new |   |
| CC       | immunotherapeutic human monoclonal antibodies. A major advantages of the  |   |
| CC       | monoclonal antibodies derives from the fact that they are encoded by a    |   |
| CC       | human polynucleotide sequence. Thus in vivo use of the monoclonal         |   |
| CC       | antibodies for diagnosis and immunotherapy of HIV induced disease greatly |   |
| CC       | reduces the problems of significant host immune response to the passively |   |
| CC       | administered antibodies which is a problem commonly encountered when      |   |
| CC       | monoclonal antibodies of xenogenic or chimeric derivation are utilized.   |   |
| CC       | An additional major advantage of the monoclonal antibodies described      |   |
| CC       | derives from the fact that they immunoreact with a unique determinant     |   |
| CC       | present on mature HIV glycoprotein gp120. This class of antibodies is     |   |
| CC       | particularly effective at neutralising field isolates of HIV.             |   |
| XX       |   |   |
| SQ       | Sequence  | 107 AA;   |
| QY       | Query Match   | 87.5%; Score 475; DB 21; Length 107;                                  |
| Dd       | Best Local Similarity   | 87.7%; Pred. No. 5.4e-29;   |
|          | Matches   | 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;                   |
| OY       | 1 ELTSPSSLSVGDRTVITSCRASORINTVTYNWQHKGKAPKLITYAASSLQGVPERF                | 60  |
|          | 1 ELTOSPSSLASVDGRTVITTCRASOSSSYTNWQQKRGKAPKLITYAASSLQGVSERF               | 60  |
| Db       | 61 SSGSGVDTFTLTISLQFEDPASYYCOESLSASATFGCGTVEIKR                           | 106   |
|          | 61 SSGSGSDTFTLTISLQPEDPATYTCQGSYSTPTTFGGTLEIKR                            | 106   |
| RESULT 5 |   |   |
| ID       | AAI98244  |   |
| AC       | AAI98244 standard; Protein; 107 AA.                                       |   |

XX 04-JUL-2000 (first entry)  
 DT Anti-gp120 antibody light chain variable region from clone b22.  
 DE  
 XX  
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;  
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;  
 KW passive immunotherapy; reduce severity; HIV-induced disease;  
 KW immunocompetence; active immunisation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN AU9948754-A.  
 XX  
 PD 17-FEB-2000.  
 XX  
 PF 16-SEP-1999; 99AU-0048754.  
 XX  
 PR 16-SEP-1999; 99AU-0048754.  
 XX  
 XX (SCRI ) SCRIpps RES INST.  
 PA  
 PI Burton DR, Barbas CF, Lerner RA;  
 DR WPI; 2000-246867/22.  
 XX  
 XX Human neutralising monoclonal antibodies to human immunodeficiency  
 PT virus (HIV) used for providing passive immunotherapy to HIV are  
 XX specific for glycoprotein-120 -  
 PS  
 PS Example 9; Figure 11; 374pp; English.  
 XX  
 CC This sequence represents a fragment of the antibodies of the invention.  
 CC The invention relates to the production of an anti-HIV (human  
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody  
 CC capable of reducing an HIV infectivity titre in an in vitro virus  
 CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The  
 CC method for the production of the antibody comprises:  
 CC (a) providing a first polynucleotide encoding a heavy chain  
 CC immunoglobulin amino acid sequence (which does not comprise the sequence  
 CC represented by AA998206) and a second polynucleotide encoding a light  
 CC chain immunoglobulin amino acid sequence;  
 CC (b) inserting the first and second polynucleotide sequences into a host  
 CC cell;  
 CC (c) maintaining the host cell in conditions which allow the amino acid  
 CC sequences encoded by the polynucleotides to be expressed in the host  
 CC cell; and  
 CC (d) isolating the antibody comprising the heavy and light chain  
 CC immunoglobulin amino acid sequences from the host cell.  
 CC The anti-HIV gp-120 monoclonal antibody is used for providing passive  
 CC immunotherapy to HIV in a human. They can be administered to high-risk  
 CC patients to reduce the likelihood and/or severity of HIV-induced disease  
 CC and to patients who are already HIV-infected. The antibodies are used  
 CC for neutralising field isolates which provides information about the  
 CC immunocompetence of an immune response in HIV patients, for detecting  
 CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
 CC producing anti-idiotypic antibodies which can be used for active  
 CC immunisation and to screen human monoclonal antibodies to identify those  
 CC with the same binding specificity and to monitor the course of HIV  
 CC disease therapy by measuring the changes in concentration of HIV present  
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120  
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and  
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
 CC reduce the problems of significant host immune response to the  
 CC antibodies associated with monoclonal antibodies of xenogeneic or  
 CC chimeric derivation.  
 CC  
 XX  
 SO Sequence 107 AA;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINTYLMWYQHKPKAKPLIYAASSLSQGVPSRF 60  
 |||||  
 DB 1 ELTQSPSSLSASVGRVITITCARASQSISSYLMWYQKPKAKPLIYAASSLSQGVPSRF 60  
 |||||  
 QY 61 SSGSGTDTFTLTITSSLSQFEDFASYYCOESLSASTYFGGCTKYEIR 106  
 |||||  
 DB 61 SSGSGTDTFTLTITSSLSQFEDFATYVCOOSYSTPTFGGCTKYEIR 106  
 |||||  
 RESULT 6  
 AAG93667  
 ID AAG93667 standard; Protein; 107 AA.  
 XX  
 AC AAG93667;  
 XX  
 DT 14-SEP-2001 (first entry)  
 XX  
 DE Human anti-Rh(D) antibody clone SH54 protein sequence.  
 XX  
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6255455-B1.  
 XX  
 PD 03-JUL-2001.  
 XX  
 PF 29-JAN-1999; 99US-0240274.  
 XX  
 PR 11-OCT-1996; 96US-0028550.  
 PR 10-APR-1998; 98US-0081380.  
 PR 27-JUN-1997; 97US-0884045.  
 XX  
 PA (TYPE-) UNIV PENNSYLVANIA.  
 PI  
 PI Siegel DL;  
 XX  
 DR WPI: 2001-388931/41.  
 DR N-PADB; AAH68724.  
 XX  
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine -  
 PS  
 PS Claim 1; Column 70; 162pp; English.  
 XX  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification  
 CC of the present invention.  
 CC  
 XX  
 SO Sequence 107 AA;

Query Match 87.3%; Score 474; DB 22; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 6 4e-29;  
 Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINTYLMWYQHKPKAKPLIYAASSLSQGVPSRF 60  
 |||||  
 DB 2 ELTQSPSSLSASVGRVITITCARASQSISSYLMWYQKPKAKPLIYAASSLSQGVPSRF 61  
 |||||  
 QY 61 SSGSGTDTFTLTITSSLSQFEDFASYYCOESLSASTYFGGCTKYEIR 106  
 |||||  
 DB 62 SSGSGTDTFTLTITSSLSQFEDFATYVCOOSYSTPTFGGCTKYEIR 107  
 |||||

|                       |   |               |
|-----------------------|---|---------------|
|                       | RESULT  | 7             |
| ID                    | AAG93590  |               |
| XX                    | AACG93590 standard; Proteoin, 107 AA.   |               |
| XX                    |   |               |
| AC                    | AAG93590;   |               |
| XX                    |   |               |
| DT                    | 14-SEP-2001   | (first entry) |
| XX                    |   |               |
| DE                    | Human anti-Rh(D) chain I02 protein sequence.  |               |
| KW                    | Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;<br>red blood cell; Rh phenotype; diagnosis; therapeutic.  |               |
| OS                    | Homo sapiens.   |               |
| XX                    |   |               |
| NB                    | US6255455-B1.   |               |
| XX                    |   |               |
| PD                    | 03-JUL-2001.  |               |
| XX                    |   |               |
| PF                    | 29-JAN-1999; 99US-0240274.  |               |
| XX                    |   |               |
| PR                    | 11-OCT-1996; 96US-0028550.<br>10-APR-1998; 98US-0081380.<br>27-JUN-1997; 97US-0884045.  |               |
| XX                    |   |               |
| PA                    | (TYPE-) UNIV PENNSYLVANIA.  |               |
| XX                    |   |               |
| F1                    | Siegel DL;  |               |
| XX                    |   |               |
| DR                    | UPI; 2001-388931/41.  |               |
| NR                    | N-PADB; AAB66647.   |               |
| XX                    |   |               |
| PT                    | New isolated proteiin, preferably a human anti-Rh(D) antibody for use in<br>diagnostics requiring a human instead of an animal antibody and in<br>therapeutic medicine -  |               |
| PS                    | Claim 1; Column 43; 162pp; English.   |               |
| CC                    | The present invention describes an isolated Rh(D) binding protein,<br>preferably a human antibody, (I) having an amino acid sequence comprising<br>one of the sequences (S) given in AACG93558 to AACG93669. (I) has<br>immunostimulant activity, and can be used as an immune system stimulant.<br>(II) can be used in diagnostic and therapeutic medicine. The antibodies<br>are used in diagnostics that require human antibodies instead of animal<br>antibodies, such as determine the Rh phenotype of human red blood cells.<br>AAB68615 to AAB68726 represent the nucleotide sequence which encode<br>AACG93558 to AACG93669. AACG93670 to AACG93697 represent anti-Rh(D) heavy<br>chain CDR3 amino acid sequences which are given in the exemplification<br>of the present invention. |               |
| Sequence              | 107 AA;   |               |
| Query Match           | 86.9%; Score 472; DB 22; Length 107;  |               |
| Best Local Similarity | 87.7%; Pred.No. 9e-29;  |               |
| Matches               | 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0,   |               |
| Oy                    | 1 ELTQPPSSLSASVGRVTITSCASQRINTLYLMNQHKGKPKLLTYASSLQGSPSRF 60<br>     ::   : :   |               |
| Dd                    | 2 ELTQPSSIISASVGRRVTTTCRASQSISISYLNNWYOOKPEKPALLITYASSLSQSVSRF 61<br>     ::   : :  |               |
| Oy                    | 61 SSGSGGTDFTLTISSLQEDFAAYYCQEBSLASATFGCGTKYEIKR 106<br>     ::   : :   |               |
| Dd                    | 62 SGSGGCTFTLTILSLQLPEDPFIATYYCQQSYSTLMTFCGCKVEIKR 107<br>     ::   : :   |               |
| RESULT                | 8   |               |
| ID                    | AAG93663  |               |
| XX                    | AACG93663 standard; Protein; 107 AA.  |               |
| XX                    |   |               |
| AC                    | AAG93663;   |               |
| XX                    |   |               |
| DT                    | 14-SEP-2001   | (first entry) |

|                       |                  |   |
|-----------------------|------------------|---|
| DE                    | XX               | Human anti-Rh(D) antibody clone SH49 protein sequence.                    |
| DE                    | XX               | Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;       |
| KW                    | XX               | red blood cell; Rh phenotype; diagnosis; therapeutic.                     |
| OS                    | XX               | Homo sapiens.   |
| XX                    | XX               | US6255455-B1.   |
| PN                    | XX               | 03-JUL-2001.  |
| PD                    | XX               | 29-JAN-1999; 99US-0240274.  |
| PF                    | XX               | 11-OCT-1996; 96US-0028550.  |
| PR                    | XX               | 10-APR-1998; 98US-0081380.  |
| PR                    | XX               | 27-JUN-1997; 97US-0884045.  |
| PA                    | XX               | (TYPE-) UNIV PENNSYLVANIA.  |
| P1                    | XX               | Siegel DL;  |
| DR                    | XX               | WPI; 2001-386931/41.  |
| DR                    | XX               | N-PSDB; AAH68720.   |
| XX                    | XX               | New isolated protein, preferably a human anti-Rh(D) antibody for use in   |
| PT                    | XX               | diagnostics requiring a human instead of an animal antibody and in        |
| PT                    | XX               | therapeutic medicine -  |
| PS                    | XX               | Claim 1; Column 69; 162pp; English.                                       |
| CC                    | XX               | The present invention describes an isolated Rh(D) binding protein,        |
| CC                    | XX               | preferably a human antibody, (I) having an amino acid sequence comprising |
| CC                    | XX               | one of the sequences (S) given in AAG93558 to AAG93669. (I) has           |
| CC                    | XX               | immunostimulant activity, and can be used as an immune system stimulant.  |
| CC                    | XX               | (I) can be used in diagnostic and therapeutic medicine. The antibodies    |
| CC                    | XX               | are used in diagnostics that require human antibodies instead of animal   |
| CC                    | XX               | antibodies, such as determine the Rh phenotype of human red blood cells.  |
| CC                    | XX               | AAH68615 to AAH68726 represent the nucleotide sequence which encode       |
| CC                    | XX               | AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy     |
| CC                    | XX               | chain CDR3 amino acid sequences which are given in the exemplification    |
| CC                    | XX               | of the present invention.   |
| SQ                    | XX               | Sequence 107 AA;  |
| Query Match           |                  | 86.9%; Score 472; DB 22; Length 107;                                      |
| Best Local Similarity |                  | 86.8%; Pred. No. 9e-29;   |
| Matches               | 92; Conservative | 7; Mismatches 7; Indels 0; Gaps 0   |
| OY                    |                  | 1 ELTSPSSLSASVGDRTVITSCRASQRIINTYINWTOHKFGKAPKLLITYASSLSQGVPSRF 60        |
| DB                    |                  | 2 ELTSPSSLSASVGDRTVITSCRASQSISSSYINWYQOKGKAPKLLITYAASSLSQGVPSRF 61        |
| OY                    |                  | 61 SGSGVGDFTLTISLOPEDFASVYCCESLSASTFGGCTVEIKR 106                         |
| DB                    |                  | 62 SGSGVGDFTLTISLOPEDFATYCCQSYSTPMTFGGCTVEIKR 107                         |
| RESULT 9              |                  |   |
| AAG93664              |                  | AAAG93664 standard; Protein; 107 AA.                                      |
| XX                    | AC               | AAAG93664;  |
| XX                    | DT               | 14-SEP-2001 (first entry)   |
| DE                    | XX               | Human anti-Rh(D) antibody clone SH50 protein sequence.                    |
| XX                    | XX               | Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;       |
| KW                    | XX               | red blood cell; Rh phenotype; diagnosis; therapeutic.                     |
| OS                    | XX               | Homo sapiens.   |
| XX                    | XX               |   |

PN US6255455-BI.  
XX  
PD 03-JUL-2001.  
XX  
PF 29-JAN-1999; 99US-0240274.  
XX  
PR 11-OCT-1996; 96US-0028550.  
PR 10-APR-1998; 98US-0081380.  
PR 27-JUN-1997; 97US-0884045.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
DR MPI: 2001-388931/41.  
DR N-PSDB; AAH68721.  
XX  
XX  
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine -  
XX  
PS Claim 1; Column 69; 162pp; English.  
XX  
XX The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
CC immunostimulant activity and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH6615 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 107 AA;  
XX  
Query Match 86.9%; Score 472; DB 22; Length 107;  
Best Local Similarity 86.8%; Pred. No. 9e-29; Indels 0; Gaps 0;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGRVTISCRASORINTYLNWYQHKPKAPKLLIYAASLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPKAPKLLIYAASLSQGVPSRF 61  
QY 61 SSGSGYGTDFTLTITSSLOFEDFASYYCOESLSASYYTFCGCTKVEIKR 106  
DB 62 SSGSGGTDFTLTITSSLOFEDFATYYCQGSYSTFWTFCGCTKVEIKR 107  
XX  
RESULT 10  
AAG93644  
ID AAG93644 standard; Protein; 107 AA.  
XX  
AC AAG93644;  
XX  
DT 14-SEP-2001 (first entry)  
XX  
DE Human anti-Rh(D) antibody clone SH3 protein sequence.  
XX  
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
XX  
OS Homo sapiens.  
XX  
PN US6255455-BI.  
XX  
PD 03-JUL-2001.  
XX  
PF 29-JAN-1999; 99US-0240274.  
XX  
PR 11-OCT-1996; 96US-0028550.  
PR 10-APR-1998; 98US-0081380.  
PR 27-JUN-1997; 97US-0884045.  
XX

PR 27-JUN-1997; 97US-0884045.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
DR MPI: 2001-388931/41.  
DR N-PSDB; AAH68701.  
XX  
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine -  
XX  
PS Claim 1; Column 68; 162pp; English.  
XX  
XX The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH6615 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 107 AA;  
XX  
Query Match 86.7%; Score 471; DB 22; Length 107;  
Best Local Similarity 86.8%; Pred. No. 1.1e-28;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGRVTISCRASORINTYLNWYQHKPKAPKLLIYAASLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPKAPKLLIYAASLSQGVPSRF 61  
QY 61 SSGSGYGTDFTLTITSSLOFEDFASYYCOESLSASYYTFCGCTKVEIKR 106  
DB 62 SSGSGGTDFTLTITSSLOFEDFATYYCQGSYSTFWTFCGCTKVEIKR 107  
XX  
RESULT 11  
AAG93593  
ID AAG93593 standard; Protein; 107 AA.  
XX  
AC AAG93593;  
XX  
DT 14-SEP-2001 (first entry)  
XX  
DE Human anti-Rh(D) chain 105 protein sequence.  
XX  
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
XX  
OS Homo sapiens.  
XX  
PN US6255455-BI.  
XX  
PD 03-JUL-2001.  
XX  
PF 29-JAN-1999; 99US-0240274.  
XX  
PR 11-OCT-1996; 96US-0028550.  
PR 10-APR-1998; 98US-0081380.  
PR 27-JUN-1997; 97US-0884045.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
DR MPI: 2001-388931/41.  
DR N-PSDB; AAH68650.  
XX

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine -  
 XX  
 XX  
 PS Claim 1; Column 44; 162pp; English.  
 CC  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (1) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG33558 to AAG33669. (1) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG33558 to AAG33669. AAG33670 to AAG33697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification  
 CC of the present invention.  
 CC  
 XX Sequence 107 AA:  
 SQ  
 Query Match 86.2%; Score 468; DB 22; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 1.8e-28;  
 Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGRVTITSCASORINTYINWQHKGKAPKLLIYAASSLSQGVSPRF 60  
 DB 2 ELTSPSSLSASVGRVTITSCASORINTYINWQHKGKAPKLLIYAASSLSQGVSPRF 61  
 QY 61 SGGSGTDTFTLTISLQFEDFASYYCOESLSASYTFGGGTVEIKR 106  
 DB 62 TCGSGGTDTFTLTISLQFEDFATYYCOGSYSTPTGCGTVEIKR 107

RESULT 12  
 AAR54261  
 ID AAR54261 standard; protein; 107 AA.  
 XX  
 AC AAR54261;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 10-NOV-1994 (first entry)  
 XX  
 DE Anti-HIV gp120 immunoglobulin light chain variable region b27.  
 XX  
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
 KW neutralisation; monoclonal antibody; kappa light chain;  
 KW variable region; framework; complementarity determining region.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..21  
 FT /label= FR1  
 FT 22..33  
 FT /label= CDR1  
 FT 34..48  
 FT /label= FR2  
 FT 49..55  
 FT /label= CDR2  
 FT 56..87  
 FT /label= FR3  
 FT 88..95  
 FT /label= CDR3  
 FT 96..107  
 FT /label= FR4  
 XX  
 XX WO9407922-A1.  
 XX 14-APR-1994.  
 PD 30-SEP-1993; 93WO-US09328.  
 XX  
 XX

PR 30-SEP-1992; 92US-0954148.  
 XX  
 XX (SCRI) SCRIPPS RES INST.  
 XX  
 PI Barbas CF, Burton DR, Lerner RA;  
 XX  
 DR WPI, 1994-135516/16.  
 XX  
 PT New human monoclonal antibodies neutralising HIV - react with  
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo  
 PT or in vitro diagnosis and for passive immuno-therapy  
 XX  
 PS Claim 5; Page 190; 248pp; English.  
 CC  
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR  
 CC amplification using primers specific for heavy and light chain  
 CC variable regions. The amplification products were inserted into a  
 CC distronic vector to produce a library of fragments. E.coli XL1  
 CC Blue cells were transformed with the library. Filamentous phage were  
 CC produced which expressed the MAb regions on their surface. Panning  
 CC with gp120 and gp41 resulted in the recovery of immunoreactive  
 CC clones. The light chain VK region sequence AAR54261 neutralises HIV1  
 CC gp120.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 107 AA:  
 SQ  
 Query Match 86.0%; Score 467; DB 15; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 2.2e-28;  
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGRVTITSCASORINTYINWQHKGKAPKLLIYAASSLSQGVSPRF 60  
 DB 1 ELTSPSSLSASVGRVTITSCASORINTYINWQHKGKAPKLLIYAASSLSQGVSPRF 60  
 QY 61 SGGSGTDTFTLTISLQFEDFASYYCOESLSASYTFGGGTVEIKR 106  
 DB 61 SGGSGTDTFTLTISLQFEDFATYYCOGSYSTPTGCGTVEIKR 106

RESULT 13  
 AAM01284  
 ID AAM01284 standard; Protein; 107 AA.  
 XX  
 AC AAM01284;  
 XX  
 DT 29-JAN-1997 (first entry)  
 DT  
 XX  
 DE VL region of HIV neutralising MAb, clone b27.  
 XX  
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;  
 KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
 KW virus infectivity assay; precursor gp160; immunocompetence; human;  
 KW anti-HIV antibody; detection; HIV infection.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..21  
 FT /label= FR1  
 FT 22..32  
 FT /label= CDR1  
 FT 33..47  
 FT /label= FR2  
 FT 48..54  
 FT /label= CDR2  
 FT 55..86  
 FT /label= FR3  
 FT 87..95  
 FT /label= CDR3  
 FT 96..107  
 FT /label= FR4  
 XX  
 XX

PN MO9602273-A1.  
 XX  
 PD 01-FEB-1996.  
 XX  
 PF 11-JUL-1995; 95MO-US08743.  
 XX  
 PR 18-JUL-1994; 94US-0276852.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 PI Barbas CF, Burton DR, Lerner RA;  
 DR WPI; 1996-179601/18.  
 XX  
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in  
 PT passive immunotherapy and detection of HIV infection.  
 XX  
 PS Example; Fig 11; 366pp; English.  
 XX  
 CC The sequences given in AAM01261-92 represent the light chain variable  
 CC regions (VL) of a series of monoclonal antibodies (Mab's) which are  
 CC immunoreactive with HIV glycoprotein gp120 and are capable of  
 CC neutralising HIV. This sequence represents the sequence of the JK2  
 CC gene clone, b27. A Mab containing this VL sequence has the capacity  
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay  
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and  
 CC binds mature gp120 preferentially over the precursor gp160. The Mab  
 CC may be used for determining immunocompetence of a human anti-HIV  
 CC antibody and in the detection of HIV infection.  
 CC  
 SQ Sequence 107 AA;  
 Query Match 86.0%; Score 467; DB 17; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 2.2e-28;  
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAKPLLIYAASSLSQGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQHKPKAKPLLIYAASSLSQGVPSRF 60  
 QY 61 SSGSGYGTDFLTITSSLSQFEDFASYYCQESLSASYTFGQGTKEIKR 106  
 DB 61 SSGSGYGTDFLTITSSLSQFEDFATYYCQGSYSTPTQTFGQGTKEIKR 106  
 RESULT 14  
 ID AAY95136  
 AC AAY95136;  
 XX  
 DT 30-JUN-2000 (first entry)  
 XX  
 DE Anti-gp120 antibody light chain variable region from clone B27.  
 XX  
 KM Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;  
 KM reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;  
 KM glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 PN AU9948756-A.  
 PD 17-FEB-2000.  
 XX  
 PF 16-SEP-1999; 99AU-0048756.  
 XX  
 PR 16-SEP-1999; 99AU-0048756.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 PI Burton DR, Barbas CF, Lerner RA;  
 XX

DR WPI; 2000-293393/26.  
 XX  
 PT Novel human monoclonal antibodies which immunoreact with and neutralise  
 PT human immunodeficiency virus useful for treating HIV infections -  
 XX  
 PS Example 9; Figure 11; 366pp; English.  
 XX  
 CC The present sequence represents a fragment of an anti-human  
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV  
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an  
 CC in vitro virus infectivity assay by 50%, at a concentration of less than  
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and  
 CC immunotherapy of HIV induced disease. They are useful as neutralising  
 CC field isolates and provide useful information regarding the  
 CC immunocompetence of an immune response in HIV infected patients. The  
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies  
 CC which can be used to screen human monoclonal antibodies to identify  
 CC whether the antibody has the same binding specificity as the antibodies  
 CC of the invention. The neutralising antibodies define new epitopes on the  
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new  
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the  
 CC monoclonal antibodies derives from the fact that they are encoded by a  
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal  
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly  
 CC reduces the problems of significant host immune response to the passively  
 CC administered antibodies which is a problem commonly encountered when  
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.  
 CC An additional major advantage of the monoclonal antibodies described  
 CC derives from the fact that they immunoreact with a unique determinant  
 CC present on mature HIV glycoprotein gp120. This class of antibodies is  
 CC particularly effective at neutralising field isolates of HIV.  
 CC  
 SQ Sequence 107 AA;  
 Query Match 86.0%; Score 467; DB 21; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 2.2e-28;  
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAKPLLIYAASSLSQGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQHKPKAKPLLIYAASSLSQGVPSRF 60  
 QY 61 SSGSGYGTDFLTITSSLSQFEDFASYYCQESLSASYTFGQGTKEIKR 106  
 DB 61 SSGSGYGTDFLTITSSLSQFEDFATYYCQGSYSTPTQTFGQGTKEIKR 106  
 RESULT 15  
 ID AAY98245  
 AC AAY98245;  
 XX  
 DT 04-JUL-2000 (first entry)  
 XX  
 DE Anti-gp120 antibody light chain variable region from clone B27.  
 XX  
 KM Antibody; anti-HIV monoclonal antibody; glycoprotein-120;  
 KM human immunodeficiency virus type 1; HIV-1; infectivity titre;  
 KM passive immunotherapy; reduce severity; HIV-induced disease;  
 KM immunocompetence; active immunisation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN AU9948754-A.  
 PD 17-FEB-2000.  
 XX  
 PF 16-SEP-1999; 99AU-0048754.  
 XX  
 PR 16-SEP-1999; 99AU-0048754.

XX (Scripps Res Inst.  
PA (Scripps Res Inst.  
...

PI Burton DR, Barbas CF, Lerner RA;

DR WPI; 2000-246867/22.

PT Human neutralizing monoclonal antibodies to human immunodeficiency virus (HIV) used for providing passive immunotherapy to HIV are specific for glycoprotein-120 -

PS Example 9; Figure 11; 374pp; English.

CC This sequence represents a fragment of the antibodies of the invention.  
CC The invention relates to the production of an anti-HIV/buffer

immunodeficiency virus) glycoprotein (gp) -120 monoclonal antibody capable of reducing an HIV infectivity titre in an in vitro virus infectivity assay by 50% at a concentration of less than 10 ng/ml. The method for the production of the antibody comprises:

CC (a) providing a first polynucleotide encoding a heavy chain  
CC immunoglobulin amino acid sequence (which does not comprise

CC represented by AY99206) and a second polynucleotide encoding a light  
CC chain immunoglobulin amino acid sequence;  
CC (b) inserting the first and second polynucleotide sequences into a host  
CC cell;

CC (c) maintaining the host cell in conditions which allow the amino acid  
CC sequences encoded by the polynucleotides to be expressed in the host

CC (d) isolating the antibody comprising the heavy and light chain  
CC immunoglobulin amino acid sequences from the host cell.

The anti-HIV gp-120 monoclonal antibody is used for providing passive immunotherapy to HIV in a human. They can be administered to high-risk patients to reduce the likelihood and/or severity of HIV-induced disease and to patients who are already HIV-infected. The antibodies are used for neutralising field isolates which provides information about the immunocompetence of an immune response in HIV patients, for detecting HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for producing anti-idiotypic antibodies which can be used for active immunisation and to screen human monoclonal antibodies to identify those with the same binding specificity and to monitor the course of HIV disease therapy by measuring the changes in concentration of HIV present in the body or in body fluids by immunoassay. The anti-HIV gp-120 monoclonal antibodies are encoded by a human polynucleotide sequence and when used in vivo for diagnosis and immunotherapy of HIV-induced disease reduce the problems of significant host immune response to the antibodies associated with monoclonal antibodies of xenogeneic or chimeric derivation.

**SQ Sequence 107 AA;**

| Query Match | Score | DB | Length |
|-------------|-------|----|--------|
| 86.0%       | 467   | 21 | 107    |

Best Local Similarity 86.8%; Pred. NO. 2.2e-28;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSSLSASVGDRVITISCRASQIRINTYLNMTQHKPGAPKLLIYAASLSQGVPSRF 600

Db 1 ELTQSSLSASVGDRVITITCRASQISISYLNMTQQKPGAPKLLIYAASLSQGVPSRF 600

Db 1 ELTQSPSSLSASVGDRVITTCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF 600

**Oy**      61 SSGSYGTDFTLTSSLOFEDPASYCQESLSASYPFGQGKVEIKR    106  
         ||||| : ||||| : ||||| : |||||  
**Db**      61 SSGSGGDFTLTISSLQPEDPATYYCCQSSTPTQTFCGGTKLEIKR    106

Db 61 SSGSGTDFLTLSLQPEDFATYYCQQSSTPQTFGQGTKLEIKR 106

Search completed: February 10, 2004, 18:36:11  
Job time : 32.9606 secs

Job time : 32.9606 secs

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RESULT 2
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:

```

```
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 313.2CON1
CURRENT APPLICATION NUMBER: US/10/016,986
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/149,898
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: US 08/899,575
PRIOR FILING DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 08/276,852
PRIOR FILING DATE: 1994-07-18
PRIOR APPLICATION NUMBER: US 08/178,302
PRIOR FILING DATE: 1994-01-06
PRIOR APPLICATION NUMBER: PCT/US93/09328
PRIOR FILING DATE: 1993-09-30
PRIOR APPLICATION NUMBER: US 07/954,148
PRIOR FILING DATE: 1992-09-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized
US-10-016-986-104
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Query Match      87.5%; Score 475; DB 12; Length 107;
Best Local Similarity 87.7%; Pred. No. 6,5e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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QY      1 ELTQSPSSLSASVGDVNTTSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      1 ELTQSPSSLSASVGDVNTTSCRASQSISSYLNWYQKPKAPKLLIYAASSLSQGVPSRF 60
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 SSGSGYDTFTLTSSLOPEDFASYCOESLSASYFGQGTKEIKR 106
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61 SSGSGYDTFTLTSSLOPEDFATYVCOOSYSTPTFTGQGTKEIKR 106
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```
RESULT 3
US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179
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Query Match      87.3%; Score 474; DB 11; Length 107;
Best Local Similarity 87.7%; Pred. No. 8.1e-38;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
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```
QY      1 ELTQSPSSLSASVGDVNTTSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
```

```
DB      2 ELTQSPSSLSASVGDVNTTSCRASQSISSYLNWYQKPKAPKLLIYAASSLSQGVPSRF 61
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 SSGSGYDTFTLTSSLOPEDFASYCOESLSASYFGQGTKEIKR 106
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      62 SSGSGYDTFTLTSSLOPEDFATYVCOOSYSTPTFTGQGTKEIKR 107
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 4
US-09-848-798-33
; Sequence 33, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33
```

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Query Match      86.9%; Score 472; DB 11; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 ELTQSPSSLSASVGDVNTTSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      2 ELTQSPSSLSASVGDVNTTSCRASQSISSYLNWYQKPKAPKLLIYAASSLSQGVPSRF 61
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 SSGSGYDTFTLTSSLOPEDFASYCOESLSASYFGQGTKEIKR 106
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      62 SSGSGYDTFTLTSSLOPEDFATYVCOOSYSTPTFTGQGTKEIKR 107
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 5
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175
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```
Query Match      86.9%; Score 472; DB 11; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-37;
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Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Query 1 ELTSPSSLSASVGDRTVITSCRASORINTYINWYOHKPKAKPLIIYAASSLSQGVPSRF 60  
Db 2 ELTSPSSLSASVGDRTVITSCRASORINTYINWYOHKPKAKPLIIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGTVEIKR 106  
Db 62 SSGSGTDFTLTISLQFEDFATYYCOOSYSTPTFGGTVEIKR 107

RESULT 6  
US-09-848-798-176  
; Sequence 176, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
US-09-848-798-176

Query Match 86.9%; Score 472; DB 11; Length 107;  
Best Local Similarity 86.8%; Pred. No. 1.3e-37;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTSPSSLSASVGDRTVITSCRASORINTYINWYOHKPKAKPLIIYAASSLSQGVPSRF 60  
Db 2 ELTSPSSLSASVGDRTVITSCRASORINTYINWYOHKPKAKPLIIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGTVEIKR 106  
Db 62 SSGSGTDFTLTISLQFEDFATYYCOOSYSTPTFGGTVEIKR 107

RESULT 7  
US-09-848-798-156  
; Sequence 156, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13  
US-09-848-798-156

Query Match 86.7%; Score 471; DB 11; Length 107;  
Best Local Similarity 86.8%; Pred. No. 1.6e-37;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTSPSSLSASVGDRTVITSCRASORINTYINWYOHKPKAKPLIIYAASSLSQGVPSRF 60  
Db 2 ELTSPSSLSASVGDRTVITSCRASORINTYINWYOHKPKAKPLIIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGTVEIKR 106  
Db 62 SSGSGTDFTLTISLQFEDFATYYCOOSYSTPTFGGTVEIKR 107

RESULT 8  
US-09-848-798-36  
; Sequence 36, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain 105  
US-09-848-798-36

Query Match 86.2%; Score 468; DB 11; Length 107;  
Best Local Similarity 86.8%; Pred. No. 3e-37;  
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTSPSSLSASVGDRTVITSCRASORINTYINWYOHKPKAKPLIIYAASSLSQGVPSRF 60  
Db 2 ELTSPSSLSASVGDRTVITSCRASORINTYINWYOHKPKAKPLIIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGTVEIKR 106  
Db 62 TSSGSGTDFTLTISLQFEDFATYYCOOSYSTPTFGGTVEIKR 107

RESULT 9  
US-10-016-986-105  
; Sequence 105, Application US/10016986  
; Publication No. US20030187247A1  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; FILE REFERENCE: 313.2CON1  
; CURRENT APPLICATION NUMBER: US/10/016,986  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 09/149,898  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: US 08/899,575  
; PRIOR FILING DATE: 1997-07-24  
; PRIOR APPLICATION NUMBER: US 08/276,852  
; PRIOR FILING DATE: 1994-07-18  
; PRIOR APPLICATION NUMBER: US 08/178,302  
; PRIOR FILING DATE: 1994-01-06

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT FILING DATE: 2001-05-04  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 37  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 106  
US-09-848-798-37

Query Match 85.5%; Score 464; DB 11; Length 107;  
Best Local Similarity 85.8%; Pred. No. 7.2e-37;  
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITTCRASQSISSYINWYQKPKKLLIYAASSLSQGVPSRF 61  
QY 61 SGGSGYGTDFLTITSSLSQEPDFASYYCOESLSASVTFGGQTKVEIKR 106  
DB 62 SGGSGGTDFLTITSSLSQEPDFATYYCQOSYSTPNTFGQTKVEIKR 107

RESULT 14  
US-09-192-854-2  
Sequence 2, Application US/09192854  
Patent No. US20020068276A1  
GENERAL INFORMATION:  
APPLICANT: Winter, Greg  
APPLICANT: Tomlinson, Ian  
TITLE OF INVENTION: Methods for Selecting Functional Peptides  
FILE REFERENCE: 3789/72916  
CURRENT FILING DATE: 1998-11-17  
EARLIER APPLICATION NUMBER: 60/066,729  
EARLIER FILING DATE: 1997-11-21  
NUMBER OF SEQ ID NOS: 212  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-192-854-2

Query Match 85.5%; Score 464; DB 9; Length 240;  
Best Local Similarity 85.8%; Pred. No. 1.7e-36;  
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 135 QMTQSPSSLSASVGDRTVITTCRASQSISSYINWYQKPKKLLIYAASSLSQGVPSRF 194  
QY 61 SGGSGYGTDFLTITSSLSQEPDFASYYCOESLSASVTFGGQTKVEIKR 106  
DB 195 SGGSGGTDFLTITSSLSQEPDFATYYCQOSYSTPNTFGQTKVEIKR 240

RESULT 15  
US-09-968-561A-2  
Sequence 2, Application US/09968561A  
Patent No. US20020164642A1  
GENERAL INFORMATION:  
APPLICANT: Tomlinson, Ian M

APPLICANT: Winter, Gregory  
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands  
FILE REFERENCE: 8039/1072B  
CURRENT FILING DATE: 2001-10-01  
PRIOR FILING DATE: 1997-10-20  
PRIOR APPLICATION NUMBER: GB 9722131.1  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: US 60/065,248  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: PCT/GB98/03135  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: US 09/511,939  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-968-561A-2

Query Match 85.5%; Score 464; DB 10; Length 240;  
Best Local Similarity 85.8%; Pred. No. 1.7e-36;  
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 135 QMTQSPSSLSASVGDRTVITTCRASQSISSYINWYQKPKKLLIYAASSLSQGVPSRF 194  
QY 61 SGGSGYGTDFLTITSSLSQEPDFASYYCOESLSASVTFGGQTKVEIKR 106  
DB 195 SGGSGGTDFLTITSSLSQEPDFATYYCQOSYSTPNTFGQTKVEIKR 240

Search completed: February 10, 2004, 19:03:03  
Job time : 24.4121 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 10.9212 Seconds  
(without alignments)  
933.402 Million cell updates/sec

Title: US-10-027-725A-10

Sequence: 1 ELTQSPSSLSASVGDRTVTS.....QESLSASYTFGGTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description               |
|------------|-------|-------------|--------|-------|---------------------------|
| 1          | 464   | 85.5        | 127    | 2     | S40367 Ig kappa chain V-J |
| 2          | 459   | 84.5        | 123    | 2     | S40331 Ig kappa chain - h |
| 3          | 458   | 84.3        | 108    | 2     | B49047 Ig kappa chain V r |
| 4          | 456   | 84.0        | 108    | 2     | S47182 Ig kappa chain - h |
| 5          | 452   | 83.2        | 109    | 2     | S31979 Ig kappa chain - h |
| 6          | 452   | 83.2        | 109    | 2     | S31998 Ig kappa chain - h |
| 7          | 448   | 82.5        | 109    | 2     | S31980 Ig kappa chain - h |
| 8          | 446   | 82.1        | 108    | 2     | S44122 Ig kappa chain V r |
| 9          | 445   | 82.0        | 109    | 2     | S32001 Ig kappa chain - h |
| 10         | 441   | 81.2        | 108    | 2     | S19674 Ig kappa chain V r |
| 11         | 439   | 80.8        | 109    | 2     | S31981 Ig kappa chain - h |
| 12         | 439   | 80.8        | 129    | 2     | S52793 Ig kappa chain V r |
| 13         | 438   | 80.7        | 107    | 2     | S36264 Ig kappa chain V   |
| 14         | 437   | 80.5        | 108    | 2     | S31977 Ig kappa chain - h |
| 15         | 436   | 80.3        | 109    | 2     | S31983 Ig kappa chain - h |
| 16         | 436   | 80.3        | 122    | 2     | S40370 Ig kappa chain - h |
| 17         | 436   | 80.3        | 129    | 1     | K1HUKK Ig kappa chain pre |
| 18         | 436   | 80.3        | 129    | 2     | S40317 Ig kappa chain - h |
| 19         | 435   | 80.1        | 128    | 2     | S46372 Ig kappa chain V-I |
| 20         | 434   | 79.9        | 120    | 2     | S46370 Ig kappa chain V-J |
| 21         | 433.5 | 79.8        | 125    | 2     | S40315 Ig kappa chain - h |
| 22         | 433   | 79.7        | 108    | 1     | K1HUKK Ig kappa chain V-I |
| 23         | 432   | 79.6        | 132    | 2     | S40334 Ig kappa chain - h |
| 24         | 431   | 79.4        | 109    | 2     | S31978 Ig kappa chain - h |
| 25         | 430   | 79.2        | 108    | 1     | K1HUKK Ig kappa chain V-I |
| 26         | 430   | 79.2        | 132    | 2     | S36646 Ig kappa chain V r |
| 27         | 425   | 78.3        | 122    | 2     | S40314 Ig kappa chain - h |
| 28         | 425   | 78.3        | 129    | 2     | S40369 Ig kappa chain - h |
| 29         | 424.5 | 78.2        | 106    | 2     | PC2397 anti-tetanus toxin |

|    |       |      |     |   |                            |
|----|-------|------|-----|---|----------------------------|
| 30 | 423.5 | 78.0 | 124 | 2 | S40336 Ig kappa chain V-J  |
| 31 | 422.5 | 77.8 | 107 | 2 | S36275 Ig lambda chain V   |
| 32 | 422   | 77.7 | 125 | 2 | S40333 Ig kappa chain V-J  |
| 33 | 422   | 77.7 | 131 | 2 | S40352 Ig kappa chain V-J  |
| 34 | 420   | 77.3 | 108 | 1 | K1HUKK Ig kappa chain V-I  |
| 35 | 420   | 77.3 | 125 | 2 | S40349 Ig kappa chain V-J  |
| 36 | 420   | 77.3 | 126 | 2 | S40350 Ig kappa chain V-J  |
| 37 | 419   | 77.2 | 125 | 2 | S40350 Ig kappa chain - h  |
| 38 | 418   | 77.0 | 117 | 2 | S546371 Ig kappa chain V-J |
| 39 | 418   | 77.0 | 129 | 2 | S52792 Ig kappa chain V r  |
| 40 | 417   | 76.8 | 117 | 2 | S46376 Ig kappa chain V-J  |
| 41 | 416   | 76.6 | 108 | 1 | K1HUKK Ig kappa chain V-I  |
| 42 | 414   | 76.2 | 107 | 2 | J10139 Ig kappa chain V r  |
| 43 | 414   | 76.2 | 107 | 2 | S36262 Ig kappa chain V r  |
| 44 | 414   | 76.2 | 108 | 1 | K1HUKK Ig lambda chain V-I |
| 45 | 413.5 | 76.2 | 108 | 2 | S30521 Ig kappa chain V r  |

## ALIGNMENTS

## RESULT 1

S40367

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40367

R:Klein, R.; Jaenichen, R.; Zachau, H. G.

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40367

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-127 <KLE>

A:Cross-references: EMBL:X72477

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 464; DB 2; Length 127;  
Best Local Similarity 84.9%; Pred. No. 4e-36;  
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

|    |    |  |                           |                   |    |
|----|----|--|---------------------------|-------------------|----|
| QY | 1  | ELTQSPSSLSASVGDRTVTS                     | CRASQRIINTYNTQHKRGP       | KLLIYAASSLSQVPSRF | 60 |
| DB | 20 | QMTQSPSSLSASVGDRTVITCRASQISINYNWYQKRGKAP | KLLIYAASSLSQVPSRF         | 79                |    |
| QY | 61 | SGSGVGFDTLTISLQEPD                       | PASYYCOESLSASYTFGGTKVEIKR | 106               |    |
| DB | 80 | SGSGGTDFTLTISLQEPD                       | PAITYCOOSYNTPTTFGGTKVEIKR | 125               |    |

## RESULT 2

S40331

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40331

R:Klein, R.; Jaenichen, R.; Zachau, H. G.

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40331

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 459; DB 2; Length 123;





R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
F:16-90/Domain: immunoglobulin homology <IMM>  
A:Accession: S31980  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
A:Cross-references: EMBL:Z15076; NID:G38491; PIDN:CAA78785.1; PID:G38492; EMBL:Z15083; N  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
Query Match 82.5%; Score 448; DB 2; Length 109;  
Best Local Similarity 81.0%; Pred. No. 1e-34;  
Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;  
Oy 2 LTQSPSSLSASVGVDRVTISCRASORINTYLNWYOHKPGKAPKLLIYAASLSQGVPSRFS 61  
Db 4 MTQSPSSLSASVGVDRVTISCRASQNIKTYLNWYOHKPGKAPKLLIYGTSTLSQGVPSRFS 63  
Oy 62 GSGGVTDFTLTISLQFEDFASVYCOESLSASVTFGGQTKVEIKR 106  
Db 64 GSGGCTDFTLTISLQFEDFATVFCQGSYSPTFFGGQTKLEIKR 108  
RESULT 8  
S44122  
Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C:Accession: S44122  
R:Hawkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable H  
A:Reference number: S44105  
A:Accession: S44122  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-108 <HAN>  
A:Cross-references: EMBL:Z31390; NID:G472976; PIDN:CAA83265.1; PID:G940533  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
Query Match 82.1%; Score 446; DB 2; Length 108;  
Best Local Similarity 83.0%; Pred. No. 1.6e-34;  
Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;  
Oy 1 ELTQSPSSLSASVGVDRVTISCRASORINTYLNWYOHKPGKAPKLLIYAASLSQGVPSRFS 60  
Db 3 QMTQSPSSLSASVGVDRVTITCRASQISISYLNWYOHKPGKAPKLLIYSSASLSQGVPSRFS 62  
Oy 61 GSGGVTDFTLTISLQFEDFASVYCOESLSASVTFGGQTKVEIKR 106  
Db 63 GSGGCTDFTLTISLQFEDFATVFCQGSYSPTFFGGQTKLEIKR 108  
RESULT 9  
S32001  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S32001  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S32001  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
A:Cross-references: EMBL:Z15082; NID:G38503; PIDN:CAA78791.1; PID:G38504

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
Query Match 82.0%; Score 445; DB 2; Length 109;  
Best Local Similarity 80.0%; Pred. No. 1.9e-34;  
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;  
Oy 2 LTQSPSSLSASVGVDRVTISCRASORINTYLNWYOHKPGKAPKLLIYAASLSQGVPSRFS 61  
Db 4 MTQSPSSLSASVGVDRVTISCRASQNIKTYLNWYOHKPGKAPKLLIYGTSTLSQGVPSRFS 63  
Oy 62 GSGGVTDFTLTISLQFEDFASVYCOESLSASVTFGGQTKVEIKR 106  
Db 64 GSGGCTDFTLTISLQFEDFATVFCQGSYSPTFFGGQTKLEIKR 108  
RESULT 10  
S19674  
Ig kappa chain V region (clone alpha-TEL9) - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C:Accession: S19674  
R:Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.  
Mol. Biol. 222, 581-597, 1991  
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph  
A:Reference number: S19663; MUID:92085276; PMID:1748994  
A:Accession: S19674  
A:Molecule type: mRNA  
A:Residues: 1-108 <MAR>  
A:Cross-references: EMBL:X61642; NID:G37860; PIDN:CAA43823.1; PID:G1335386  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
Query Match 81.2%; Score 441; DB 2; Length 108;  
Best Local Similarity 82.9%; Pred. No. 4.5e-34;  
Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;  
Oy 2 LTQSPSSLSASVGVDRVTISCRASORINTYLNWYOHKPGKAPKLLIYAASLSQGVPSRFS 61  
Db 4 LTQSPSSLSASVGVDRVTITCRASQISISYLNWYOHKPGKAPKLLIYAASLSQGVPSRFS 63  
Oy 62 GSGGVTDFTLTISLQFEDFASVYCOESLSASVTFGGQTKVEIKR 106  
Db 64 GSGGCTDFTLTISLQFEDFATVFCQGSYSPTFFGGQTKLEIKR 108  
RESULT 11  
S31981  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S31981  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S31981  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
A:Cross-references: EMBL:Z15077; NID:G38493; PIDN:CAA78786.1; PID:G38494  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
Query Match 80.8%; Score 439; DB 2; Length 109;  
Best Local Similarity 80.0%; Pred. No. 7e-34;  
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;  
Oy 2 LTQSPSSLSASVGVDRVTISCRASORINTYLNWYOHKPGKAPKLLIYAASLSQGVPSRFS 61  
Db 4 MTQSPSSLSASVGVDRVTITCRASQISISYLNWYOHKPGKAPKLLIYSSASLSQGVPSRFS 62

Db 4 MTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKGKAPKLLIHGASTLBSGVPSRFS 63  
 QY 62 GSGYGTDFTLTITSSLOPEDFASYYCOESLSASTFGCGTKVEIKR 106  
 64 GSGSGTDFLTITSSLOPEDFATYYCOQSYSTPFTFGGKLEIKR 108

## RESULT 12

S52793  
 Ig kappa chain V region - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 19-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
 C/Accession: S52793  
 R/Rocca, A.; Khamilchi, A.A.; Touchard, G.; Mounenot, B.; Ronco, P.; Denotoy, L.; Deret, submitted to the EMBL Data Library, March 1995  
 A/Description: Light chain V region gene usage restriction and peculiarities in myeloma-  
 A/Reference number: S52789  
 A/Accession: S52793  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-129 <ROC>  
 A/Cross-references: EMBL:X65997; NID:G758600; PIDN:CAA59989.1; PID:G758601  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:18-112/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 129;  
 Best Local Similarity 81.9%; Pred. No. 8.3e-34;  
 Matches 86; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPKGKAPKLLIYAASLSQSGVPSR 60  
 25 QMTQSPSSLSASVGDRTVITCRASQNIISTYLMWYQKPKGKAPKLLIYAASLSQSGVPSR 84  
 Db 61 GSGYGTDFTLTITSSLOPEDFASYYCOESLSASTFGCGTKVEIKR 105  
 85 GSGSGTDFLTITSSLOPEDFATYYCOQYSAPELTFGCGTKVEIKR 129

## RESULT 13

S36264  
 Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
 C/Accession: S36264  
 R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; EMO J. 12, 725-734, 1993  
 A/Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A/Reference number: S36256; MUID:93178448; EUID:7679990  
 A/Accession: S36264  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-107 <GRI>  
 A/Cross-references: EMBL:Z18845; NID:G33426; PIDN:CAA79297.1; PID:G939919  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 438; DB 2; Length 107;  
 Best Local Similarity 83.7%; Pred. No. 8.5e-33;  
 Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPKGKAPKLLIYAASLSQSGVPSRFS 61  
 4 LTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPKGKAPKLLIYAASLSQSGVPSRFS 63  
 Db 62 GSGYGTDFTLTITSSLOPEDFASYYCOESLSASTFGCGTKVEIKR 105  
 64 GSGSGTDFLTITSSLOPEDFATYYCOQSYNPLTFGGTKVNDIK 107

## RESULT 14

S31977

Ig kappa chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-2001  
 C/Accession: S31977  
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992  
 A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
 A/Reference number: S31977  
 A/Accession: S31977  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-108 <POR>  
 A/Cross-references: EMBL:Z15073  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 437; DB 2; Length 108;  
 Best Local Similarity 82.9%; Pred. No. 1.1e-33;  
 Matches 87; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPKGKAPKLLIYAASLSQSGVPSRFS 61  
 4 MTQSPSSLSASVGDRTVITCRASQSIISYLMWYQKPKGKAPKLLIYAASLSQSGVPSRFS 63  
 Db 62 GSGYGTDFTLTITSSLOPEDFASYYCOESLSASTFGCGTKVEIKR 106  
 64 GSGSGTDFLTITSSLOPEDFATYYCOQSYDTDTGHTGKVEIKR 108

## RESULT 15

S31983  
 Ig kappa chain - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C/Accession: S31983  
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992  
 A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
 A/Reference number: S31977  
 A/Accession: S31983  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-109 <POR>  
 A/Cross-references: EMBL:Z15073; NID:G38497; PIDN:CAA78788.1; PID:G38498  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 436; DB 2; Length 109;  
 Best Local Similarity 79.0%; Pred. No. 1.3e-33;  
 Matches 83; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPKGKAPKLLIYAASLSQSGVPSRFS 61  
 4 MTQSPSSLSASVGDRTVITCRASQSIISYLMWYQKPKGKAPKLLIYAASLSQSGVPSRFS 63  
 Db 62 GSGYGTDFTLTITSSLOPEDFASYYCOESLSASTFGCGTKVEIKR 106  
 64 GSGGTDFLTITSSLOPEDFATYYCOQSYSSPYTFGCGTKLEIKR 108

Search completed: February 10, 2004, 18:41:10  
 Job time: 11.9212 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 ; Search time 5.94242 Seconds  
(without alignments)  
838.855 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543  
Sequence: 1 ELTGSPSSLSASVGDRTVIS.....QESLSASTYFGQTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 436   | 80.3        | 129    | 1 KVIW_HUMAN | P04431 homo sapien |
| 2          | 433   | 79.7        | 108    | 1 KVIK_HUMAN | P01597 homo sapien |
| 3          | 430   | 79.2        | 108    | 1 KVIH_HUMAN | P01600 homo sapien |
| 4          | 420   | 77.3        | 108    | 1 KVIH_HUMAN | P01606 homo sapien |
| 5          | 416   | 76.6        | 108    | 1 KVIK_HUMAN | P01598 homo sapien |
| 6          | 414   | 76.2        | 108    | 1 KVIK_HUMAN | P01603 homo sapien |
| 7          | 413   | 76.1        | 108    | 1 KVIH_HUMAN | P01607 homo sapien |
| 8          | 412   | 75.9        | 108    | 1 KVIH_HUMAN | P01599 homo sapien |
| 9          | 409   | 75.3        | 108    | 1 KVIH_HUMAN | P01605 homo sapien |
| 10         | 408   | 75.1        | 108    | 1 KVIH_HUMAN | P01594 homo sapien |
| 11         | 407   | 75.0        | 108    | 1 KVIH_HUMAN | P01610 homo sapien |
| 12         | 406   | 74.8        | 108    | 1 KVIH_HUMAN | P01593 homo sapien |
| 13         | 404   | 74.4        | 108    | 1 KVIH_HUMAN | P01596 homo sapien |
| 14         | 399.5 | 73.6        | 107    | 1 KVID_HUMAN | P01611 homo sapien |
| 15         | 399   | 73.5        | 108    | 1 KVIH_HUMAN | P01608 homo sapien |
| 16         | 398   | 73.3        | 108    | 1 KVIH_HUMAN | P01604 homo sapien |
| 17         | 397   | 73.1        | 129    | 1 KVIH_HUMAN | P04432 homo sapien |
| 18         | 396   | 72.9        | 108    | 1 KVIH_HUMAN | P01609 homo sapien |
| 19         | 391   | 72.0        | 108    | 1 KVIH_HUMAN | P01612 homo sapien |
| 20         | 385.5 | 71.0        | 109    | 1 KVIH_HUMAN | P01595 homo sapien |
| 21         | 384   | 70.7        | 108    | 1 KVIH_HUMAN | P01653 mus musculu |
| 22         | 376   | 69.2        | 108    | 1 KVIH_HUMAN | P01653 mus musculu |
| 23         | 373   | 68.2        | 108    | 1 KVIH_HUMAN | P01653 mus musculu |
| 24         | 370.5 | 68.2        | 109    | 1 KVIH_HUMAN | P01650 mus musculu |
| 25         | 370   | 68.1        | 108    | 1 KVIH_HUMAN | P01622 homo sapien |
| 26         | 368.5 | 67.9        | 109    | 1 KVIH_HUMAN | P01622 homo sapien |
| 27         | 368   | 67.9        | 109    | 1 KVIH_HUMAN | P01647 mus musculu |
| 28         | 368   | 67.8        | 108    | 1 KVIH_HUMAN | P01647 mus musculu |
| 29         | 368   | 67.8        | 108    | 1 KVIH_HUMAN | P01647 mus musculu |
| 30         | 368   | 67.8        | 108    | 1 KVIH_HUMAN | P01647 mus musculu |
| 31         | 367.5 | 67.7        | 129    | 1 KVIH_HUMAN | P18136 homo sapien |
| 32         | 367.5 | 67.7        | 129    | 1 KVIH_HUMAN | P18136 homo sapien |
| 33         | 366.5 | 67.5        | 129    | 1 KVIH_HUMAN | P18135 homo sapien |

|    |     |      |     |              |                    |
|----|-----|------|-----|--------------|--------------------|
| 34 | 366 | 67.4 | 114 | 1 KVIH_HUMAN | P01625 homo sapien |
| 35 | 366 | 67.4 | 117 | 1 KVIH_HUMAN | P01601 homo sapien |
| 36 | 365 | 67.2 | 108 | 1 KVIH_HUMAN | P01644 mus musculu |
| 37 | 365 | 67.2 | 108 | 1 KVIH_HUMAN | P01646 mus musculu |
| 38 | 365 | 67.2 | 134 | 1 KVIH_HUMAN | P06314 homo sapien |
| 39 | 364 | 67.0 | 108 | 1 KVIH_HUMAN | P01651 mus musculu |
| 40 | 363 | 66.9 | 111 | 1 KVIH_HUMAN | P01665 mus musculu |
| 41 | 362 | 66.7 | 111 | 1 KVIH_HUMAN | P01664 mus musculu |
| 42 | 361 | 66.5 | 108 | 1 KVIH_HUMAN | P01645 mus musculu |
| 43 | 360 | 66.3 | 108 | 1 KVIH_HUMAN | P01645 mus musculu |
| 44 | 358 | 65.9 | 111 | 1 KVIH_HUMAN | P01667 mus musculu |
| 45 | 357 | 65.7 | 128 | 1 KVIH_HUMAN | P01637 mus musculu |

ALIGNMENTS

| RESULT 1 | ID   | KVIH_HUMAN                        | STANDARD  | PRT | 129 AA                            |
|----------|--|-----------------------------------|-----------|-----|-----------------------------------|
| AC       | P04431   |                                   |           |     |                                   |
| DT       | 13-AUG-1987  | (Rel. 05, Created)                |           |     |                                   |
| DT       | 13-AUG-1987  | (Rel. 05, Last sequence update)   |           |     |                                   |
| DT       | 15-JUL-1999  | (Rel. 38, Last annotation update) |           |     |                                   |
| DE       | Ig kappa chain V-I region Walker precursor.  |                                   |           |     |                                   |
| OS       | Homo sapiens (Human).  |                                   |           |     |                                   |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                                   |           |     |                                   |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo;  |                                   |           |     |                                   |
| OX       | NCBI_TaxID=9606;   |                                   |           |     |                                   |
| RN       | [1]  |                                   |           |     |                                   |
| RP       | SEQUENCE FROM N.A.   |                                   |           |     |                                   |
| RX       | MEDLINE=85014148; PubMed=6091049;  |                                   |           |     |                                   |
| RA       | Klobeck H.G., Combrato G., Zachau H.G.;  |                                   |           |     |                                   |
| RT       | "Immunoglobulin genes of the kappa light chain type from two human   |                                   |           |     |                                   |
| RT       | lymphoid cell lines are closely related."  |                                   |           |     |                                   |
| RL       | Nucleic Acids Res. 12:6995-7006(1984).   |                                   |           |     |                                   |
| CC       | -----  |                                   |           |     |                                   |
| CC       | This SWISS-PROT entry is copyright. It is produced through a collaboration   |                                   |           |     |                                   |
| CC       | between the Swiss Institute of Bioinformatics and the EMBL outstation -  |                                   |           |     |                                   |
| CC       | the European Bioinformatics Institute. There are no restrictions on its  |                                   |           |     |                                   |
| CC       | use by non-profit institutions as long as its content is in no way   |                                   |           |     |                                   |
| CC       | modified and this statement is not removed. Usage by and for commercial  |                                   |           |     |                                   |
| CC       | entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> |                                   |           |     |                                   |
| CC       | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |                                   |           |     |                                   |
| CC       | -----  |                                   |           |     |                                   |
| DR       | EMBL; X00965; CAA25477.1; ALT_TERM.  |                                   |           |     |                                   |
| DR       | PIR; A01883; K1H7MK.   |                                   |           |     |                                   |
| DR       | HSSP; P01607; IREI.  |                                   |           |     |                                   |
| DR       | GO; GO:0005576; C:extracellular; NAS.  |                                   |           |     |                                   |
| DR       | GO; GO:0003823; F:antigen binding activity; NAS.   |                                   |           |     |                                   |
| DR       | GO; GO:0006955; F:immune response; NAS.  |                                   |           |     |                                   |
| DR       | InterPro; IPR007110; Ig-like.  |                                   |           |     |                                   |
| DR       | InterPro; IPR003006; Ig MHC.   |                                   |           |     |                                   |
| DR       | InterPro; IPR003596; Ig_V.   |                                   |           |     |                                   |
| DR       | Pfam; PF00047; Ig_1.   |                                   |           |     |                                   |
| DR       | SMART; SM00406; IGV_1.   |                                   |           |     |                                   |
| DR       | PROSITE; PS50835; IG_LIKE; 1.  |                                   |           |     |                                   |
| KW       | Immunoglobulin V region, Signal.   |                                   |           |     |                                   |
| FT       | SIGNAL   | 1                                 | 22        |     | IG KAPPA CHAIN V-I REGION WALKER. |
| FT       | CHAIN  | 23                                | 129       |     | FRAMEWORK-1.                      |
| FT       | DOMAIN   | 23                                | 45        |     | COMPLEMENTARITY-DETERMINING-1.    |
| FT       | DOMAIN   | 46                                | 56        |     | FRAMEWORK-2.                      |
| FT       | DOMAIN   | 57                                | 71        |     | COMPLEMENTARITY-DETERMINING-2.    |
| FT       | DOMAIN   | 72                                | 78        |     | FRAMEWORK-3.                      |
| FT       | DOMAIN   | 79                                | 110       |     | COMPLEMENTARITY-DETERMINING-3.    |
| FT       | DOMAIN   | 111                               | 119       |     | FRAMEWORK-4.                      |
| FT       | DOMAIN   | 120                               | 129       |     | BY SIMILARITY.                    |
| FT       | DISTUFD  | 45                                | 110       |     |                                   |
| FT       | NON_TER  | 129                               | 129       |     |                                   |
| SQ       | SEQUENCE   | 129 AA;                           | 14069 MW; |     | F941FA07D4AFC2F9 CRC64;           |

Query Match 80.3%; Score 436; DB 1; Length 129;  
Best Local Similarity 81.9%; Pred. No. 6,1e-40;

Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASQRIINTYLNWYOHKPKGAPKLLIYAASSLSQGVPSRF 60  
 DB 25 QMTQSPSSLSASVGDVITITCRASQSIINTYLNWYOHKPKGAPKLLIYAASSLSQGVPSRF 84  
 QY 61 SSGSGYDTFTLTITSSLOFEDFASVYCOESLSASVYTCGCTKVEIKR 105  
 DB 65 SSGSGYDTFTLTITSSLOFEDFASVYTCGCTKVEIKR 129

## RESULT 2

KVLE HUMAN  
 ID KVLE HUMAN STANDARD; PRT; 108 AA.

AC P01567;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region DEB.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RX MEDLINE=72053133; PubMed=5124396;  
 RP "The amino acid sequence of a human kappa light chain."  
 RT Blochem. J. 123:945-958(1971).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR; A01865; KIHUDE.  
 DR HSSP; P01607; 1REI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IgV\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 FRAMEWORK-2.  
 FT DOMAIN 35 49 FRAMEWORK-3.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11661 MW; BDDEE350017FIE51 CRC64;

Query Match 79.7%; Score 433; DB 1; Length 108;

Best Local Similarity 77.4%; Pred. No. 1e-39;  
 Matches 82; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASQRIINTYLNWYOHKPKGAPKLLIYAASSLSQGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDVITITCRASQSIINTYLNWYOHKPKGAPKLLIYAASSLSQGVPSRF 62  
 QY 61 SSGSGYDTFTLTITSSLOFEDFASVYCOESLSASVYTCGCTKVEIKR 106  
 DB 63 SSGSGYDTFTLTITSSLOFEDFASVYTCGCTKVEIKR 108

## RESULT 3

KVH HUMAN  
 ID KVH HUMAN STANDARD; PRT; 108 AA.

AC P01600;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Hau.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RX MEDLINE=71032830; PubMed=4097974;

RP SEQUENCE.  
 RA Matnabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups."  
 RT Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR; A01868; KIHOU.  
 DR HSSP; P80362; 1WTU.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IgV\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones Protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 FRAMEWORK-2.  
 FT DOMAIN 35 49 FRAMEWORK-3.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.2%; Score 430; DB 1; Length 108;

Best Local Similarity 78.3%; Pred. No. 2.2e-39;  
 Matches 83; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASQRIINTYLNWYOHKPKGAPKLLIYAASSLSQGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDVITITCRASQSIINTYLNWYOHKPKGAPKLLIYAASSLSQGVPSRF 62  
 QY 61 SSGSGYDTFTLTITSSLOFEDFASVYCOESLSASVYTCGCTKVEIKR 106  
 DB 63 SSGSGYDTFTLTITSSLOFEDFASVYTCGCTKVEIKR 108

## RESULT 4

KVIN HUMAN  
 ID KVH HUMAN STANDARD; PRT; 108 AA.

AC P01606;  
 DT 21-JUL-1986 (Rel. 01, Created).  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region OU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RX MEDLINE=70201507; PubMed=5447531;

RP SEQUENCE.  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;  
 RT "Macroglobulin structure: variable sequence of light and heavy chains."  
 RT Science 169:56-59(1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.

```

DR PIR: A01872; KIHOU.
DR HSSP: P01607; IREI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA424105827E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 2,6e-38;
Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTYISCRASQRIINTYIMVYQHKRGKAPKLLIYAASLSQGVPSRF 60
DB 3 QMTZSPSLSSASVGBRVITTCRASZTISSYLWYZZKRGKAPBLIYAASLSQGVPSRF 62
QY 61 SSGSGTDFLTITSLQFEDPASYCOESLSASYTFGGGTVEIK 106
DB 63 SSGSGTDFLTITSLQFEDPASYCOESLSASYTFGGGTVEIK 108

RESULT 5
KV1F_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR: A01869; KIHUKA.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSSP: P80362; IWTU.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839F8BD542F4B CRC64;

Query Match 76.2%; Score 414; DB 1; Length 108;
Best Local Similarity 70.8%; Pred. No. 1,2e-37;

```

```

DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 76.6%; Score 416; DB 1; Length 108;
Best Local Similarity 77.1%; Pred. No. 7e-38;
Matches 81; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTYISCRASQRIINTYIMVYQHKRGKAPKLLIYAASLSQGVPSRF 60
DB 3 QMTZSPSLSSASVGBRVITTCRASQRIINTYIMVYQHKRGKAPKLLIYAASLSQGVPSRF 62
QY 61 SSGSGTDFLTITSLQFEDPASYCOESLSASYTFGGGTVEIK 105
DB 63 IGGSGTDFLTITSLQFEDPASYCOESLSASYTFGGGTVEIK 107

RESULT 6
KV1K_HUMAN STANDARD; PRT; 108 AA.
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR: A01869; KIHUKA.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSSP: P80362; IWTU.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839F8BD542F4B CRC64;

Query Match 76.2%; Score 414; DB 1; Length 108;
Best Local Similarity 70.8%; Pred. No. 1,2e-37;

```

Matches 75; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSSSSLSASGVDRVTISCRASQRIINTLYNMYQKPGAPRLLYAASSLOSQVPSRP 60  
 DB 3 QMTQSPSTLSVSGDRTITTCENASQTVLSTLYNMYQKPGAPRLLYAASSLETGVPSRP 62

QY 61 SSGSGYGTDFLTITSSLOFEDFASVYCOESLSASVTFQGTKEIKR 106  
 DB 63 SSGSGSTBFTFTTISVYZPZBFATYYCOZYLDLPRTGQGTKEIKR 108

RESULT 7  
 KVI10 HUMAN  
 ID KVI10 HUMAN STANDARD; PRT; 108 AA.

AC P04430;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region BAN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=66174817; PubMed=3083240;  
 RA Dwulet F.E., O'Connor T.P., Benson M.D.;  
 RT "Polymorphism in a kappa I primary (AI) amyloid protein (BAN).";  
 RL Mol. Immunol. 23:73-78(1986).  
 DR PIR; A01878; KIHUBN.  
 DR HSSP; P80362; 1MTL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Amyloid.  
 KW DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 24 34 FRAMEWORK-2.  
 FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 50 56 FRAMEWORK-3.  
 FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 89 97 FRAMEWORK-4.  
 FT DOMAIN 98 107 BY SIMILARITY.  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 76.1%; Score 413; DB 1; Length 108;  
 Best Local Similarity 76.4%; Pred. No. 1.5e-37;  
 Matches 81; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSSSSLSASGVDRVTISCRASQRIINTLYNMYQKPGAPRLLYAASSLOSQVPSRP 60  
 DB 3 QMTQSPSTLSVSGDRTITTCENASQTVLSTLYNMYQKPGAPRLLYAASSLETGVPSRP 62

QY 61 SSGSGYGTDFLTITSSLOFEDFASVYCOESLSASVTFQGTKEIKR 106  
 DB 63 SSGSGSTBFTFTTISVYZPZBFATYYCOZYLDLPRTGQGTKEIKR 108

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=76023758; PubMed=8093329;  
 RA Palm W., Hilschmann N.;  
 RT "The primary structure of a crystalline monoclonal immunoglobulin  
 kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation  
 and characterization of the tryptic peptides; the complete amino acid  
 sequence of the protein; a contribution to the elucidation of the  
 three-dimensional structure of antibodies, in particular their  
 combining site.";  
 RT Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
 RL [2]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RP MEDLINE=76039968; PubMed=1182131;  
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;  
 RT "The molecular structure of a dimer composed of the variable portions  
 of the Bence-Jones protein REI refined at 2.0-A resolution.";  
 RL Biochemistry 14:493-495(1975).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A91663; KIHURE.  
 DR PDB; 1REI; 17-FEB-84.  
 DR PDB; 1AR2; 12-NOV-97.  
 DR PDB; 1BMW; 29-DEC-99.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 KW DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 24 34 FRAMEWORK-2.  
 FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 50 56 FRAMEWORK-3.  
 FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 89 97 FRAMEWORK-4.  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT TURN 15 16  
 FT STRAND 19 25  
 FT TURN 30 31  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 44 49  
 FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT TURN 76 77  
 FT HELIX 80 82  
 FT STRAND 85 90  
 FT STRAND 97 98  
 FT STRAND 102 106  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11902 MW; 9EB143E118BCE2A CRC64;

Query Match 75.9%; Score 412; DB 1; Length 108;  
 Best Local Similarity 75.5%; Pred. No. 1.9e-37;  
 Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITISCRASORINTYLMWYOHKPKAPKLLIYAASSLSQGVPSRF 60  
 DB 3 QMTOSPSLSASVGRVITITCOASODITKYLNMWYQOTGKAPKLLIYASNLQAGVPSRF 62  
 QY 61 SSGSGVGTDTFTLTISLQFEDFASYYCOESLSASYTFGGGTVEIKR 106  
 DB 63 SSGSGGTDTFTLTISLQFEDFATYTCQYQSLPYFGGTVEIKR 108

## RESULT 9

KVIG\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01559;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Gal.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCB1\_Taxid=9606;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=75059122; PubMed=4215718;  
 RA Laure C.J., Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal IgM-immunoglobulin  
 (macroglobulin Gal.), I. The amino acid sequence of the L-chain of  
 kappa-type, subgroup I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 MACROGLOBULIN.

DR PIR; A01867; KIHUGL.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region.  
 KM DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 24 34 FRAMEWORK-2.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 75.3%; Score 409; DB 1; Length 108;  
 Best Local Similarity 78.3%; Pred. No. 4e-37;  
 Matches 83; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITISCRASORINTYLMWYOHKPKAPKLLIYAASSLSQGVPSRF 60  
 DB 3 QMTOSPSLSASVGRVITITCOASODITKYLNMWYQOTGKAPKLLIYASNLQAGVPSRF 62  
 QY 61 SSGSGVGTDTFTLTISLQFEDFASYYCOESLSASYTFGGGTVEIKR 106  
 DB 63 SSGSGGTDTFTLTISLQFEDFATYTCQYQSLPYFGGTVEIKR 108

RESULT 10  
 KVIM\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01605;  
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Lay.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCB1\_Taxid=9606;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=77038198; PubMed=824717;  
 RA Capra J.D., Klappper D.G.;  
 RT "Complete amino acid sequence of the variable domains of two human  
 RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic  
 RT specificities.";  
 RL Stand. J. Immunol. 5:677-684(1976).  
 CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS  
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN PGM V-II KAPPA CHAIN,  
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
 CC GLOBULIN ACTIVITY.

DR PIR; A01871; KIHULY.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region.  
 KM DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 24 34 FRAMEWORK-2.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 75.1%; Score 408; DB 1; Length 108;  
 Best Local Similarity 73.6%; Pred. No. 5.1e-37;  
 Matches 78; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITISCRASORINTYLMWYOHKPKAPKLLIYAASSLSQGVPSRF 60  
 DB 3 QMTOSPSLSASVGRVITITCOASONVANYLMWYQOKGAPKLLIYASLRAGVPSRF 62  
 QY 61 SSGSGVGTDTFTLTISLQFEDFASYYCOESLSASYTFGGGTVEIKR 106  
 DB 63 SSGSGGTDTFTLTISLQFEDFATYTCQYQNMWYPTFGGTVEIKR 108

## RESULT 11

KVIB\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01554;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-I region AU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCB1\_Taxid=9606;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA Schiehl H., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal

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RT Immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au.);
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RX X-RAY CRYSTALLOGRAPHY.
RA MEDLINE=77022433; PubMed=1234024;
RA Fehlfamer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A91653; KIHUW.
DR PDB; 1JVS; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E801187E6F6FB9 CRC64;

Query Match 75.8%; Score 407; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 6.5e-37;
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSISASVGDRTVITSCRASQRIINTYLNWYQHKPKGAPKLLIYAASLSQGVPSRF 60
DB 3 QMTQSSSSISASVGDRTVITSCRASQDISDLYNQYQKPGAPKLLIYDSSNESGVPSRF 62
DB 63 SGGSGGSHFTFTISSIQPEDIAITYCQYDYLPTFGQGTKEIKR 108

RESULT 12
KVIR_HUMAN STANDARD; PRT; 108 AA.
ID KVIR_HUMAN
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (prolein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY

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CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC PIR; A01876; KIHUWE.
DR HSSP; P80362; 1WTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Monoclonal antibody.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 74.8%; Score 406; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 8.3e-37;
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSISASVGDRTVITSCRASQRIINTYLNWYQHKPKGAPKLLIYAASLSQGVPSRF 60
DB 3 QMTQSSSSISASVGDRTVITSCRASQIRNDLTYWQKPGTAPKRLIYGATSSQGVPSRF 62
DB 61 SSGSGGTDTFTLTSSIQPEDFASVYCOESLSASYFGQGTKEIKR 106
DB 63 SSGSGGTDTFTLTSSIQPEDFATYCYCQYDYLPTFGQGTKEIKR 108

RESULT 13
KVIA_HUMAN STANDARD; PRT; 108 AA.
ID KVIA_HUMAN
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence and the location of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01861; KIHUAG.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

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FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 74.4%; Score 404; DB 1; Length 108;  
 Best Local Similarity 73.6%; Pred. No. 1.4e-36;  
 Matches 78; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITSCRASORINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 60  
 DB 3 QMTOSPSLSASVGRVITTCASQDINHLYNMYQOGPKKAPKLLIYASNLLETVPSPRF 62  
 QY 61 SSGSGGTDFTLTISLSQFEDFASYYCOESLSASTYFGGCTVKEIKR 106  
 DB 63 SSGSGGTDFTLTISLSQFEDFATYFCQYDTLPRTFGGCTVKEIKR 108

## RESULT 14

KVID HUMAN STANDARD; PRT; 107 AA.  
 AC P01596;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region CAR.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75075135; PubMed=4216454;  
 RA Milstein C.P.; Deverson E.V.;  
 RT "Primary structure of kappa light chain from a human myeloma protein."  
 RT Eur. J. Biochem. 49:377-391(1974).  
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR; A01864; KIHUAR.  
 DR HSSP; P80362; 1WTL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Glycoprotein.  
 KW CARBOHYD 28  
 FT NON TER 107 107  
 FT SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match 73.6%; Score 399.5; DB 1; Length 107;  
 Best Local Similarity 71.7%; Pred. No. 4.1e-36;  
 Matches 76; Conservative 18; Mismatches 11; Indels 1; Gaps 1;

QY 1 ELTOSPSLSASVGRVITSCRASORINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 60  
 DB 3 QMTOSPSLSASVGRVITTCASQDINHLYNMYQOGPKKAPKLLIYASNLLETVPSPRF 62  
 QY 61 SSGSGGTDFTLTISLSQFEDFASYYCOESLSASTYFGGCTVKEIKR 106  
 DB 63 SSGSGGTDFTLTISLSQFEDFATYFCQYDTLPRTFGGCTVKEIKR 107

RESULT 15  
 KVID HUMAN STANDARD; PRT; 108 AA.  
 AC P01611;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Wes.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81092279; PubMed=6778806;  
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;  
 RT "Preparative separation of the tryptic hydrolyzate of a protein by high-pressure liquid chromatography. The primary structure of a monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes)."  
 RT Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).  
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
 DR PIR; A01877; KIHUWS.  
 DR HSSP; P80362; 1WTL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 24 33 FRAMEWORK-1.  
 FT DOMAIN 24 35 49 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 50 56 FRAMEWORK-2.  
 FT DOMAIN 50 57 88 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 89 97 FRAMEWORK-3.  
 FT DOMAIN 89 98 107 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 FT SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 73.5%; Score 399; DB 1; Length 108;  
 Best Local Similarity 73.6%; Pred. No. 4.7e-36;  
 Matches 78; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITSCRASORINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 60  
 DB 3 QMTOSPSLSASVGRVITTCASQDINHLYNMYQOGPKKAPKLLIYASNLLETVPSPRF 62  
 QY 61 SSGSGGTDFTLTISLSQFEDFASYYCOESLSASTYFGGCTVKEIKR 106  
 DB 63 SSGSGGTDFTLTISLSQFEDFATYFCQYDTLPRTFGGCTVKEIKR 108

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Db 3 QMTQSPSSLSASVGDRTTTCRASQSISSYLNWYQOKPGKAPNLLIYAASLSQGVPSRF 62

QY 61 SSGGYGTDFTLTITSSIQFEDFASYYCOESLSASYTGCGTKVEIKR 106  
 |||||  
 63 SSGSGTDFLTITSSIQFEDFATYYCOQSYSTSWTGEKTKVEIKR 108

## RESULT 2

Q96SA9 PRELIMINARY; PRT; 107 AA.

AC Q96SA9; PRELIMINARY; PRT; 107 AA.

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain

DE Variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=98375893; PubMed=9712075;

RT Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;

RT "Molecular analysis of polyclonal antibodies from

RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin

RT antibody V region genes."

RT J. Immunol. 161:2020-2031(1998).

RL EMBL; U96396; AAB68785.1; -

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_v.

DR Pfam: PF00047; IG\_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1 1

FT NON\_TER 107 107

SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 82.8%; Score 449.5; DB 4; Length 107;

Best Local Similarity 84.9%; Pred. No. 4.6e-42;

Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQOKPGKAPNLLIYAASLSQGVPSRF 60

Db 3 QMTQSPSSLSASVGDRTTTCRASQSISSYLNWYQOKPGKAPNLLIYAASLSQGVPSRF 62

QY 61 SSGGYGTDFTLTITSSIQFEDFASYYCOESLSASYTGCGTKVEIKR 106

Db 63 SSGSGTDFLTITSSIQFEDFATYYCOQSYSTSWTGEKTKVEIKR 108

RESULT 3

Q9UL81 PRELIMINARY; PRT; 107 AA.

AC Q9UL81; PRELIMINARY; PRT; 107 AA.

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DE Myosin-reactive immunoglobulin light chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RA MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus."

RT Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035033; AAD56269.1; -

DR HSSP; P01607; IREI.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_v.

DR Pfam; PF00047; IG\_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1 1

FT NON\_TER 107 107

SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 80.9%; Score 439.5; DB 4; Length 107;

Best Local Similarity 82.1%; Pred. No. 5.9e-41;

Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQOKPGKAPNLLIYAASLSQGVPSRF 60

Db 3 QMTQSPSSLSASVGDRTTTCRASQSISSYLNWYQOKPGKAPNLLIYAASLSQGVPSRF 62

QY 61 SSGGYGTDFTLTITSSIQFEDFASYYCOESLSASYTGCGTKVEIKR 106

Db 63 SSGSGTDFLTITSSIQFEDFATYYCOQSYSTSWTGEKTKVEIKR 108

RESULT 4

Q9UL79 PRELIMINARY; PRT; 108 AA.

AC Q9UL79; PRELIMINARY; PRT; 108 AA.

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DE Myosin-reactive immunoglobulin light chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=98277139; PubMed=9614934;

RT Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus."

RT Clin. Immunol. Immunopathol. 87:184-192(1998).

QL Clin. Immunol. Immunopathol. 87:184-192(1998).

QY 2 LTQSPSSLSASVGDRTTTCRASQSISSYLNWYQOKPGKAPNLLIYAASLSQGVPSRF 61

Db 4 MTQSPSSLSASVGDRTTTCRASQSISSYLNWYQOKPGKAPNLLIYAASLSQGVPSRF 63

QY 62 SSGGYGTDFTLTITSSIQFEDFASYYCOESLSASYTGCGTKVEIKR 106

Db 64 SSGSGTDFLTITSSIQFEDFATYYCOQSYSTSWTGEKTKVEIKR 108

RESULT 5

Q9UL70

ID 09UL70 PRELIMINARY; PRT; 108 AA.  
AC 09UL70;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035044; AAD56280.1; -.  
DR HSSP; P01607; IRET.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 77.3%; Score 420; DB 4; Length 108;  
Best Local Similarity 79.2%; Pred. No. 8,6e-39;  
Matches 84; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGRVITSCASORINTYLMWYOHKPKAPKLIYAASLSQSVPSRF 60  
Db 3 QMTQSPSSLSASVGRVITTCASQGISNYLAWYQKRGKPKSLIYAASLSQSVPSRF 62  
Qy 61 SGGSGYTDFTLTISLQFEDFASYYCOESLSASYTFGGTKEIKR 106  
Db 63 SGGSGYTDFTLTISLQFEDFATYCCQKNSAPRTFGGTKEIKR 108

RESULT 6  
Q9UL83 PRELIMINARY; PRT; 108 AA.  
ID 09UL83;  
AC 09UL83;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035031; AAD56267.1; -.  
DR HSSP; P80362; IMTL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92BBA6EEA CRC64;  
Query Match 68.3%; Score 371; DB 4; Length 108;  
Best Local Similarity 65.7%; Pred. No. 2,3e-33;  
Matches 69; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGRVITSCASORINTYLMWYOHKPKAPKLIYAASLSQSVPSRF 61  
Db 4 MTQSPATLSPGGRATLSCASQSVSSNLAWYQKRGKAPRLIYCASTATGTPARFS 63  
Qy 62 SGGSGYTDFTLTISLQFEDFASYYCOESLSASYTFGGTKEIKR 106  
Db 64 SGGSGYTDFTLTISLQFEDFATYCCQKNSAPRTFGGTKEIKR 108

RESULT 7  
Q96PF6 PRELIMINARY; PRT; 116 AA.  
ID 096PF6;  
AC 096PF6;  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Kappa 1 light chain variable region (Fragment).  
CN SDKL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21361171; PubMed=11468171;  
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;  
RT "The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell burden";  
RL Blood 98:714-720(2001).  
DR EMBL; AF361758; AAKS1465.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 68.3%; Score 371; DB 4; Length 116;  
Best Local Similarity 67.9%; Pred. No. 2,5e-33;  
Matches 72; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGRVITSCASORINTYLMWYOHKPKAPKLIYAASLSQSVPSRF 60  
Db 3 QMTQSPSSLSASVGRVITTCASQGISNYLAWYQKRGKAPKLIYAASLSQSVPSRF 62  
Qy 61 SGGSGYTDFTLTISLQFEDFASYYCOESLSASYTFGGTKEIKR 106  
Db 63 SGGSGATNFTLTISLQFEDFATYCCQYHHLPTFGGTKEIKR 108

RESULT 8  
Q9OYF0 PRELIMINARY; PRT; 298 AA.  
ID 09OYF0;  
AC 09OYF0;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE CN 8 scFv.  
CN CN 8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RX NCBI\_TaxId=10090;  
 OX  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BaIb/c; TISSUE=Spleen;  
 RX MEDLINE=20183931; PubMed=10706631;  
 RA Shinohara N., Demura T., Fukuda H.;  
 RT "Isolation of a vascular cell wall-specific monoclonal antibody  
 RT recognizing a cell polarity by using a phase display subtraction  
 RT method.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).  
 DR EMBL; AB036341; BAA88633.1; -  
 DR HSSP; P01607; IRE1.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SMO0406; IGV; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 SQ SEQUENCE 298 AA; 31667 MW; E0F96BBA17004317 CRC64;  
 Query Match 67.4%; Score 366; DB 11; Length 298;  
 Best Local Similarity 67.0%; Pred. No. 2,9e-32;  
 Matches 71; Conservative 13; Mismatches 22; Indels 0; Gaps 0;  
 OY 1 ELTQSPSSLSASVGRVITISCSASQRIINTYLMWYHKKGAKPKLLIYAASSLSQGVPSRF 60  
 DB 175 ELTQSPASSLSASVGTVTITTCASGNHNYLAWYQKQKSPQLLVYNAKTLADGVPSRF 234  
 OY 61 SGGSGVDTFTLTISLQFEDFPASYCCQESLSAYFGQGTKEIKR 106  
 DB 235 SGGSGGTQYSLKINSLOPEDFESYTCQHFMTTPTYFGGTKEIKR 280  
 RESULT 9  
 O9RIAS  
 ID O9RIAS PRELIMINARY; PRT; 214 AA.  
 AC O9RIAS.  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Kappa light chain of Mab7 (Fragment).  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
 RT antibody (Mab 7, its light and heavy chains) and construction of a  
 RT single chain antibody (scFv).";  
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF152371; AAD40242.1; -  
 DR HSSP; P01679; 2F8T.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; PM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 FT NON\_TER  
 FT TER 1  
 SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;  
 Query Match 67.0%; Score 364; DB 11; Length 214;  
 Best Local Similarity 64.2%; Pred. No. 3.2e-32;  
 Matches 68; Conservative 18; Mismatches 20; Indels 0; Gaps 0;  
 OY 1 ELTQSPSSLSASVGRVITISCSASQRIINTYLMWYHKKGAKPKLLIYAASSLSQGVPSRF 60  
 DB 3 QLTQSPSSWYASLGERVITITTCASQDINSYLSWFOQKQKSPKLLIYRANRLVDGVPSRF 62

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Oy      61  SGSGSGVDFLTITSLQFEDPASYYCOESLSASTFGCGKVEIKR 106
        |||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      63  SGSGSGGVDFLTITSLQFEDPASYYCOESLSASTFGCGKVEIKR 108

RESULT 10
O91MP8  O91MP8      PRELIMINARY;      PRT;      234 AA.
ID      ID
AC      O91MP8;
DT      01-DEC-2001 (TReMBLrel. 19, Created)
DT      01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      Hypothetical 25.9 kDa protein.
OS      Mus musculus (Mouse).
OC      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
OC      Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Colon;
RA      Strausberg R.;
RL      Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC015292; AAH1529.1; -.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      InterPro; IPR001865; Ribosomal_S2.
DR      Pfam; PF00047; IG; 2.
DR      SMART; SM00406; IG; 1.
DR      PROSITE; PS00290; IG_MHC; 1.
DR      PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
SQ      Hypothetical protein.
      SEQUENCE      234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match      66.5%; Score 361; DB 11; Length 234;
Best Local Similarity 65.1%; Pred. No. 7.6e-32;
Matches 69; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

Oy      1  ELTQSPSLASVGDRTYISCRASQRINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60
        :::::|||||:::|||||:::|||||:::|||||:::|||||
Db      23  QMTDTTSSLSASLGRRTISCRASQDLSNLTNMYQKPKDGTVKLLIYTRLYIGVSRF 82
        |||||:::|||||:::|||||:::|||||:::|||||

Oy      61  SGSGSGVDFLTITSLQFEDPASYYCOESLSASTFGCGKVEIKR 106
        |||||:::|||||:::|||||:::|||||:::|||||
Db      83  SGSGSGGVDFLTITSLQFEDPASYYCOESLSASTFGCGKVEIKR 128
        |||||:::|||||:::|||||:::|||||:::|||||

RESULT 11
O9R062  O9R062      PRELIMINARY;      PRT;      234 AA.
ID      ID
AC      O9R062;
DT      01-JUN-2002 (TReMBLrel. 21, Created)
DT      01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      Hypothetical 25.9 kDa protein.
OS      Mus musculus (Mouse).
OC      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
OC      Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Colon;
RA      Strausberg R.;
RL      Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC027418; AAH27418.1; -.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; IG; 2.
DR      SMART; SM00406; IG; 1.
DR      PROSITE; PS00835; IG LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; 1.
SQ      Hypothetical protein.

```

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SO SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;
Query Match 66.5%; Score 361; DB 11; Length 234;
Best Local Similarity 67.0%; Pred. No. 7,6e-32;
Matches 71; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITSCRASQRIINTYLNWYOHKRGKAPKLLIYAASSLSQSGVPSRF 60
Db 23 QMTQSPASLASVGEVITTCRASGNLHNYLAWYQOKGSPOLLVYNAKTLADGVPSRF 82
Qy 61 SSGSGYDTFTLTISLSQFEDPFASYCOESLSASYTFGGGTVEIKR 106
Db 83 SSGSGGTHTSLTISLNPEDPATYTCQYQSGPFTFGGTLEIKR 128

RESULT 12
Q8NEK1 PRELIMINARY; PRT; 234 AA.
ID Q8NEK1
AC Q8NEK1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030813; AAH30813.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00407; IGV_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25530 MW; 6316B8DEFD132F8 CRC64;

Query Match 66.3%; Score 360; DB 4; Length 234;
Best Local Similarity 64.8%; Pred. No. 9,8e-32;
Matches 68; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

Qy 2 LTQSPSSLASVGDRTVITSCRASQRIINTYLNWYOHKRGKAPKLLIYAASSLSQSGVPSRF 61
Db 24 MTQSPATLSVSPGERATLISCRASQSVNTSLAWYQQTPOSPLVLYGASSRAGVPARFS 83
Qy 62 GSGYDTFTLTISLSQFEDPFASYCOESLSASYTFGGGTVEIKR 106
Db 84 GSGGTHTSLTISLNPEDPATYTCQYQSGPFTFGGTLEIKR 128

RESULT 13
Q920E6 PRELIMINARY; PRT; 109 AA.
ID Q920E6
AC Q920E6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307938; AAL09422.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98B05DD1501 CRC64;

Query Match 66.1%; Score 359; DB 11; Length 109;
Best Local Similarity 65.1%; Pred. No. 4,9e-32;
Matches 69; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITSCRASQRIINTYLNWYOHKRGKAPKLLIYAASSLSQSGVPSRF 60
Db 3 QMTQSPASLASVGEVITTCRASGNLHNYLAWYQOKGSPOLLVYNAKTLADGVPSRF 62
Qy 61 SSGSGYDTFTLTISLSQFEDPFASYCOESLSASYTFGGGTVEIKR 106
Db 63 SSGSGGTHTSLTISLNPEDPATYTCQYQSGPFTFGGTLEIKR 108

RESULT 14
Q920E9 PRELIMINARY; PRT; 111 AA.
ID Q920E9
AC Q920E9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA685836 CRC64;

Query Match 66.1%; Score 359; DB 11; Length 111;
Best Local Similarity 63.9%; Pred. No. 5e-32;
Matches 69; Conservative 16; Mismatches 19; Indels 4; Gaps 1;

Qy 2 LTQSPSSLASVGDRTVITSCRASQRIINTYLNWYOHKRGKAPKLLIYAASSLSQSGVPSRF 57
Db 4 LTQSPASLASVGEVITTCRASQSVNTSLAWYQQTPOSPLVLYGASSRAGVPARFS 63
Qy 58 SRPFGSGYDTFTLTISLSQFEDPFASYCOESLSASYTFGGGTVEIKR 105
Db 64 ARPFGSGYDTFTLTINHPVEDPATYTCQYQSGPFTFGGTLEIKR 111

RESULT 15
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ID 091WS9      PRELIMINARY;      PRT:      233 AA.
AC 091WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AH13496.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PR00047; ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
FT NON TER
SQ SEQUENCE      233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match      65.7%; Score 357; DB 11; Length 233;
Best Local Similarity 67.0%; Pred. No. 2.1e-31;
Matches 71; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASGVDRVTISCRASORINTYLNWYQHKPKAKPLIYAASLSQGVPSRF 60
DB 22 QMTQTTSLSASLGDRVTISCSGSGIANTLNMWYQQKPDGTVKLIYITSSLSHSGVPSRF 81

QY 61 SSGSGYTDFTLTITSLQFEDFASVYCOESLSASVTFGGTKVEIKR 106
DB 82 SSGSGSGTDYSLTISNLEPEDIAITYCQQRVYLPMTFGGTKEIKR 127

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Search completed: February 10, 2004, 18:39:22  
 Job time : 26.0545 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 ; Search time 10.9212 Seconds

(without alignments)  
410.664 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543  
Sequence: 1 ELTQSPSSLSASVGDRTYIS.....QESLSASTFGQTKVRIKR 106Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A COMB.pdp:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B COMB.pdp:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A COMB.pdp:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B COMB.pdp:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS COMB.pdp:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfilest.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                   | Description       |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1          | 475   | 87.5        | 107    | 1 US-08-276-852-104  | Sequence 104, App |
| 2          | 475   | 87.5        | 107    | 1 US-08-899-575-104  | Sequence 104, App |
| 3          | 475   | 87.5        | 107    | 1 US-08-899-575-104  | Sequence 104, App |
| 4          | 475   | 87.5        | 107    | 5 PCT-US95-08743-104 | Sequence 104, App |
| 5          | 474   | 87.3        | 107    | 3 US-09-240-274-179  | Sequence 179, App |
| 6          | 472   | 86.9        | 107    | 3 US-09-240-274-33   | Sequence 33, App1 |
| 7          | 472   | 86.9        | 107    | 3 US-09-240-274-175  | Sequence 175, App |
| 8          | 472   | 86.9        | 107    | 3 US-09-240-274-176  | Sequence 176, App |
| 9          | 471   | 86.7        | 107    | 3 US-09-240-274-156  | Sequence 156, App |
| 10         | 468   | 86.2        | 107    | 3 US-09-240-274-36   | Sequence 36, App1 |
| 11         | 467   | 86.0        | 107    | 1 US-08-276-852-105  | Sequence 105, App |
| 12         | 467   | 86.0        | 107    | 1 US-08-899-575-105  | Sequence 105, App |
| 13         | 467   | 86.0        | 107    | 1 US-08-899-575-105  | Sequence 105, App |
| 14         | 467   | 86.0        | 107    | 5 PCT-US95-08743-105 | Sequence 105, App |
| 15         | 464.5 | 85.5        | 108    | 3 US-09-240-274-32   | Sequence 32, App1 |
| 16         | 464.5 | 85.5        | 108    | 3 US-09-240-274-43   | Sequence 43, App1 |
| 17         | 464   | 85.1        | 107    | 3 US-09-240-274-37   | Sequence 37, App1 |
| 18         | 462   | 85.1        | 107    | 3 US-09-240-274-38   | Sequence 38, App1 |
| 19         | 462   | 85.1        | 107    | 3 US-09-240-274-39   | Sequence 39, App1 |
| 20         | 461   | 84.9        | 107    | 3 US-09-240-274-158  | Sequence 158, App |
| 21         | 460.5 | 84.8        | 108    | 3 US-09-240-274-167  | Sequence 167, App |
| 22         | 459.5 | 84.6        | 108    | 3 US-09-240-274-163  | Sequence 163, App |
| 23         | 458   | 84.3        | 107    | 3 US-09-240-274-35   | Sequence 35, App1 |
| 24         | 458   | 84.3        | 107    | 3 US-09-240-274-173  | Sequence 173, App |
| 25         | 457   | 84.2        | 104    | 1 US-08-379-057-29   | Sequence 29, App1 |
| 26         | 457   | 84.2        | 104    | 1 US-08-276-852-106  | Sequence 106, App |
| 27         | 457   | 84.2        | 104    | 1 US-08-899-575-106  | Sequence 106, App |

|    |       |      |     |                      |                   |
|----|-------|------|-----|----------------------|-------------------|
| 28 | 457   | 84.2 | 104 | 1 US-08-899-575-106  | Sequence 106, App |
| 29 | 457   | 84.2 | 104 | 5 PCT-US95-08743-106 | Sequence 106, App |
| 30 | 457   | 84.2 | 107 | 3 US-09-240-274-40   | Sequence 40, App1 |
| 31 | 456   | 84.0 | 107 | 3 US-09-240-274-44   | Sequence 44, App1 |
| 32 | 452   | 83.2 | 107 | 3 US-09-240-274-172  | Sequence 172, App |
| 33 | 452   | 83.2 | 107 | 3 US-09-240-274-174  | Sequence 174, App |
| 34 | 451.5 | 83.1 | 108 | 1 US-08-276-852-109  | Sequence 109, App |
| 35 | 451.5 | 83.1 | 108 | 1 US-08-899-575-109  | Sequence 109, App |
| 36 | 451.5 | 83.1 | 108 | 1 US-08-899-575-109  | Sequence 109, App |
| 37 | 451.5 | 83.1 | 108 | 3 US-09-240-274-41   | Sequence 41, App1 |
| 38 | 451.5 | 83.1 | 108 | 5 PCT-US95-08743-109 | Sequence 109, App |
| 39 | 451   | 83.1 | 107 | 3 US-09-240-274-168  | Sequence 168, App |
| 40 | 451   | 83.1 | 108 | 4 US-09-025-7698-14  | Sequence 14, App1 |
| 41 | 451   | 83.1 | 109 | 2 US-07-934-373C-3   | Sequence 3, App1  |
| 42 | 451   | 83.1 | 109 | 3 US-08-437-642B-3   | Sequence 3, App1  |
| 43 | 451   | 83.1 | 109 | 4 US-08-146-206C-3   | Sequence 3, App1  |
| 44 | 451   | 83.1 | 109 | 5 PCT-US93-07832-3   | Sequence 3, App1  |
| 45 | 450   | 82.9 | 107 | 3 US-09-240-274-34   | Sequence 34, App1 |

## ALIGNMENTS

RESULT 1  
US-08-276-852-104  
Sequence 104, Application US/08276852  
Patent No. 5652138  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Bardas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESS: Patent Counsel  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 7e-39;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINLYNMWYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGRVITITCRASQSISSYLMWYQOKPKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDTFTLTISLQFEDFASYYCOESLSASYTGQGTKEIKR 106  
DB 61 SSGSGTDTFTLTISLQPEDFATYYCQOSYSTPYTFGQGTKEIKR 106

RESULT 2  
US-08-899-575-104  
; Sequence 104, Application US/08899575

; Patent No. 5770440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Letner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRI452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 7e-39;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINLYNMWYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGRVITITCRASQSISSYLMWYQOKPKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDTFTLTISLQFEDFASYYCOESLSASYTGQGTKEIKR 106  
DB 61 SSGSGTDTFTLTISLQPEDFATYYCQOSYSTPYTFGQGTKEIKR 106

RESULT 3  
US-08-899-575-104  
; Sequence 104, Application US/08899575

; Patent No. 5804440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Letner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRI452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 7e-39;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINLYNMWYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGRVITITCRASQSISSYLMWYQOKPKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDTFTLTISLQFEDFASYYCOESLSASYTGQGTKEIKR 106  
DB 61 SSGSGTDTFTLTISLQPEDFATYYCQOSYSTPYTFGQGTKEIKR 106

RESULT 4  
PCT-US95-08743-104  
; Sequence 104, Application PC/TUS9508743

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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match      87.5%; Score 475; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 7e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQKRGKAPKLLIYAASSLSQGVPSRF 60

Cy 61 SSGSGYDTFTLTISLQFEDPASYCCOESLSASYTFGGGTVEIKR 106
Db 61 SSGSGYDTFTLTISLQFEDPATYCCOQSYSTPTFFGGTVEIKR 106

Db 62 SSGSGYDTFTLTISLQFEDPATYCCOQSYSTPTFFGGTVEIKR 106

RESULT 5
US-09-240-274-179
; Sequence 179, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match      87.3%; Score 474; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 8.7e-39;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQKRGKAPKLLIYAASSLSQGVPSRF 61

Cy 61 SSGSGYDTFTLTISLQFEDPASYCCOESLSASYTFGGGTVEIKR 106
Db 62 SSGSGYDTFTLTISLQFEDPATYCCOQSYSTPTFFGGTVEIKR 107
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RESULT 6
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQKRGKAPKLLIYAASSLSQGVPSRF 61

Cy 61 SSGSGYDTFTLTISLQFEDPASYCCOESLSASYTFGGGTVEIKR 106
Db 62 SSGSGYDTFTLTISLQFEDPATYCCOQSYSTPTFFGGTVEIKR 107

RESULT 7
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.4e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQKRGKAPKLLIYAASSLSQGVPSRF 61
```



FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-105

Query Match 86.0%; Score 467; DB 1; Length 107;  
Best Local Similarity 86.8%; Pred. No. 4.1e-38;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVISCRAQORINTYLNWYQHKPKAKPKLLIYAASSLSGVSFRF 60  
Db 1 ELTQSPSLASVGDRTVITCRASQSISSYLNWYQHKPKAKPKLLIYAASSLSGVSFRF 60

Qy 61 SSGSGYDFTLTITISLQFEDFASYYCOESLSASTPFGGTVEIKR 106  
Db 61 SSGSGYDFTLTITISLQFEDFATYYCOQSYSTPQTFGGTVEIKR 106

RESULT 12  
US-08-899-575-105  
Sequence 105, Application US/08899575  
Patent No. 5770440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
STREET: Mail Drop 7PC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Query Match 86.0%; Score 467; DB 1; Length 107;  
Best Local Similarity 86.8%; Pred. No. 4.1e-38;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVISCRAQORINTYLNWYQHKPKAKPKLLIYAASSLSGVSFRF 60  
Db 1 ELTQSPSLASVGDRTVITCRASQSISSYLNWYQHKPKAKPKLLIYAASSLSGVSFRF 60

Qy 61 SSGSGYDFTLTITISLQFEDFASYYCOESLSASTPFGGTVEIKR 106  
Db 61 SSGSGYDFTLTITISLQFEDFATYYCOQSYSTPQTFGGTVEIKR 106

RESULT 13  
US-08-899-575-105  
Sequence 105, Application US/08899575  
Patent No. 5804440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
STREET: Mail Drop 7PC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Query Match  
Best Local Similarity 86.0%; Score 467; DB 1; Length 107;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTISCRASORINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPSRF 60  
QY 61 SSGSGTDPFTLTISLQFDPFASYCOESLSASTTGCGTKVEIKR 106  
DB 61 SSGSGTDPFTLTISLQFDPFATYCCOQSYSTPQTFGQGTKEIKR 106

## RESULT 14

PCT-US95-08743-105  
Sequence 105, Application PC/TUS9508743

## GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
NUMBER OF INVENTIONS: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08743  
FILING DATE: 11-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-08743-105

Query Match  
Best Local Similarity 86.0%; Score 467; DB 5; Length 107;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTISCRASORINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPSRF 60  
QY 61 SSGSGTDPFTLTISLQFDPFASYCOESLSASTTGCGTKVEIKR 106  
DB 61 SSGSGTDPFTLTISLQFDPFATYCCOQSYSTPQTFGQGTKEIKR 106

## RESULT 15

US-09-240-274-32  
Sequence 32, Application US/09240274

## GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09396-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 32

LENGTH: 108  
TYPE: PRP

ORGANISM: Homo sapiens  
FEATURE:

OTHER INFORMATION: anti-Rh(D) chain 101  
US-09-240-274-32

Query Match  
Best Local Similarity 85.5%; Score 464.5; DB 3; Length 108;  
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGRVTISCRASORINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGTDPFTLTISLQFDPFASYCOESLSASTTGCGTKVEIKR 106  
DB 62 SSGSGTDPFTLTISLQFDPFATYCCOQSYSTPQTFGQGTKEIKR 108

Search completed: February 10, 2004, 18:42:08  
Job time: 11.9212 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 10.9212 Seconds

(without alignments)  
933.402 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547  
Sequence: 1 ELTQSPSSLSASVGDRTVIT.....QOSTTLYTPSGTKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : PIR 76:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID  | Description        |
|------------|-------|---------|--------------|--------|--------------------|
| 1          | 468   | 85.6    | 108          | B49047 | Ig kappa chain V r |
| 2          | 465   | 85.0    | 108          | S47182 | Ig kappa chain - h |
| 3          | 465   | 85.0    | 127          | S40367 | Ig kappa chain V-J |
| 4          | 464   | 84.8    | 109          | S31998 | Ig kappa chain - h |
| 5          | 462   | 84.5    | 123          | S40331 | Ig kappa chain - h |
| 6          | 457   | 83.5    | 122          | S40370 | Ig kappa chain - h |
| 7          | 455   | 83.2    | 108          | S44122 | Ig kappa chain V r |
| 8          | 454   | 83.0    | 108          | S31977 | Ig kappa chain - h |
| 9          | 453   | 82.8    | 129          | K1HUMK | Ig kappa chain pre |
| 10         | 451   | 82.4    | 109          | S31981 | Ig kappa chain - h |
| 11         | 451   | 82.4    | 109          | S31978 | Ig kappa chain - h |
| 12         | 449   | 82.1    | 108          | K1HUMD | Ig kappa chain V-I |
| 13         | 447   | 81.7    | 108          | S19674 | Ig kappa chain V r |
| 14         | 446   | 81.5    | 129          | S40317 | Ig kappa chain - h |
| 15         | 438   | 80.1    | 117          | S46371 | Ig kappa chain V-J |
| 16         | 437.5 | 80.0    | 106          | PC2397 | anti-tetanus toxin |
| 17         | 437   | 79.9    | 107          | S36264 | Ig lambda chain V  |
| 18         | 437   | 79.9    | 108          | K1HUMU | Ig kappa chain V-I |
| 19         | 437   | 79.9    | 120          | S46370 | Ig kappa chain V-J |
| 20         | 436   | 79.7    | 109          | S31979 | Ig kappa chain V-J |
| 21         | 434   | 79.3    | 129          | S52793 | Ig kappa chain V r |
| 22         | 433   | 79.2    | 128          | S46372 | Ig light chain var |
| 23         | 432   | 79.0    | 109          | S31980 | Ig kappa chain - h |
| 24         | 432   | 79.0    | 125          | S40350 | Ig kappa chain - h |
| 25         | 431   | 78.8    | 109          | S31983 | Ig kappa chain - h |
| 26         | 429   | 78.4    | 129          | S52792 | Ig kappa chain V r |
| 27         | 429   | 78.4    | 132          | S40334 | Ig kappa chain - h |
| 28         | 428   | 78.2    | 109          | S32001 | Ig kappa chain - h |
| 29         | 428   | 78.2    | 122          | S40314 | Ig kappa chain - h |

|    |       |      |     |   |        |                    |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 428   | 78.2 | 132 | 2 | S38646 | Ig kappa chain V r |
| 31 | 427.5 | 78.2 | 125 | 2 | S40315 | Ig kappa chain - h |
| 32 | 427   | 78.1 | 125 | 2 | S40349 | Ig kappa chain V-J |
| 33 | 425.5 | 77.8 | 124 | 2 | S40336 | Ig kappa chain V-J |
| 34 | 424.5 | 77.6 | 107 | 2 | S36275 | Ig kappa chain V   |
| 35 | 424   | 77.5 | 108 | 1 | K1HUMU | Ig kappa chain V-I |
| 36 | 424   | 77.5 | 125 | 2 | S40333 | Ig kappa chain V-J |
| 37 | 421.5 | 77.1 | 108 | 2 | S30521 | Ig kappa chain V r |
| 38 | 419   | 76.6 | 116 | 2 | A27594 | Ig kappa chain pre |
| 39 | 419   | 76.6 | 117 | 2 | S24206 | Ig kappa chain V r |
| 40 | 418   | 76.4 | 109 | 2 | JN0296 | Ig kappa chain V-J |
| 41 | 418   | 76.4 | 129 | 2 | S40369 | Ig kappa chain - h |
| 42 | 417.5 | 76.3 | 108 | 2 | S34007 | Ig kappa chain V r |
| 43 | 417   | 76.2 | 126 | 2 | S40335 | Ig kappa chain V-J |
| 44 | 416   | 76.1 | 108 | 1 | K1HUMU | Ig kappa chain V-I |
| 45 | 416   | 76.1 | 108 | 1 | K1HUMK | Ig kappa chain V-I |

#### ALIGNMENTS

##### RESULT 1

B49047  
Ig kappa chain V region (monoclonal strictional autoantibody Strab SA-1A) - human (fragm  
C:Species: Homo sapiens (man)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: B49047  
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A:Title: Human monoclonal strictional autoantibodies isolated from thymic B lymphocytes  
A:Reference number: A49047; MUID:92387224; PMID:1516616  
A:Accession: B49047  
A:Status: Preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-108 <VIC>  
A:Experimental source: thymic B lymphocytes  
A:Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:113209)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 85.6%; Score 468; DB 2; Length 108;  
Query 1 ELTQSPSSLSASVGDRTVITTCRAQISITINWYQKRGKAPKLLMSASNLQSGVPSRF 60  
Db 3 QMTQSPSSLSASVGDRTVITTCRAQISITINWYQKRGKAPKLLIYAAASLQSGVPSRF 62  
Matches 90; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 61 SGSGSGTEFTLTISNLOPEDPASYYCOOSYTTLYTPSGTKLEIKR 106  
Db 63 SGSGSGTDFLTITISLQPEDPATYYCOOSYSTPLTFGSGTKLEIKR 108

##### RESULT 2

S47182  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S47182  
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.  
submitted to the EMBL Data Library, June 1994  
A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient  
A:Reference number: S47181  
A:Accession: S47182  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-108 <MCI>  
A:Cross-references: EMBL:X79786; NID:G506422; PIDD:CA56182.1; PIDD:G506423  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 465; DB 2; Length 108;





R.Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A:Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable  
A:Reference number: S44105  
A:Accession: S44122  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-108 <HAM>  
A:Cross-references: EMBL:Z31390; NID:G472976; PIN:CAA83265.1; PID:G940533  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 455; DB 2; Length 108;  
Best Local Similarity 84.0%; Pred. No. 8.8e-35;  
Matches 89; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60  
:::|||||  
DB 3 QMTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPKAKPLIYASLSQSGVPSRF 62  
:::|||||

QY 61 GSGSGTEFTLTISNLOPEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
|||||  
DB 63 GSGSGTDFTLTISLQPEDFAIYYCOQSYSTPMTFGQTKVEIKR 108  
|||||

RESULT 8  
S31977  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-2001  
C:Accession: S31977  
R.Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S31977  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-108 <POR>  
A:Cross-references: EMBL:Z15073  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 454; DB 2; Length 108;  
Best Local Similarity 84.8%; Pred. No. 1.1e-34;  
Matches 89; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 61  
:::|||||  
DB 4 MTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPKAKPLIYASLSQSGVPSRF 63  
:::|||||

QY 62 GSGSGTEFTLTISNLOPEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
|||||  
DB 64 GSGSGTDFTLTISLQPEDFAIYYCOQSYSTPMTFGQTKVEIKR 108  
|||||

RESULT 9  
K1HUNK  
Ig kappa chain precursor V-I region (Walker) - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 21-Jan-2000  
C:Accession: A01883  
R.Klobeck, H.G.; Combrat, G.; Zachau, H.G.  
Nucleic Acids Res. 12, 6995-7006, 1984  
A:Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell  
A:Reference number: A93534; MUID:85014148; PMID:6091049  
A:Accession: A01883  
A:Molecule type: DNA  
A:Residues: 1-129 <KLO>  
A>Note: the sequence was determined from the differentiated gene  
C:Genetics:

A:Gene: GDB:IGKVL  
A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:23-129/Product: Ig kappa chain V-I region (Walker) #status predicted <MAT>  
F:23-45/Region: Framework 1  
F:38-112/Domain: immunoglobulin homology <IMM>  
F:46-56/Region: complementarity-determining 1  
F:57-71/Region: Framework 2  
F:72-78/Region: complementarity-determining 2  
F:79-110/Region: Framework 3  
F:111-119/Region: complementarity-determining 3  
F:120-129/Region: Framework 4  
F:45-110/Disulfide bonds: #status predicted

Query Match 82.8%; Score 453; DB 1; Length 129;  
Best Local Similarity 83.8%; Pred. No. 1.6e-34;  
Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60  
:::|||||  
DB 25 QMTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPKAKPLIYASLSQSGVPSRF 84  
:::|||||

QY 61 GSGSGTEFTLTISNLOPEDFASYYCOQSYTTLTYFGSGTKLEIKR 105  
|||||  
DB 85 GSGSGTDFTLTISLQPEDSATYYCOQSYSTPMTFGQTKLEIKR 129  
|||||

RESULT 10  
S31981  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S31981  
R.Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S31981  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
A:Cross-references: EMBL:Z15077; NID:G38493; PIN:CAA78786.1; PID:G38494  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 451; DB 2; Length 109;  
Best Local Similarity 82.9%; Pred. No. 2.1e-34;  
Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 61  
:::|||||  
DB 4 MTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQOKPKAKPLIYASLSQSGVPSRF 63  
:::|||||

QY 62 GSGSGTEFTLTISNLOPEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
|||||  
DB 64 GSGSGTDFTLTISLQPEDFAIYYCOQSYSTPMTFGQTKLEIKR 108  
|||||

RESULT 11  
S31978  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S31978  
R.Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

```

A:Reference number: S31977
A:Accession: S31978
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <POS>
A:Cross-references: EMBL:J15074; NID:g38487; PID:CAA76783.1; PID:g38488
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      82.4%; Score 451; DB 2; Length 109;
Best Local Similarity 82.9%; Pred. No. 2,1e-34;
Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTGSPSSISASVGRVTTCRARGISITLYLNWYQKPKAPKLIIWSASNIQSVPSPRS 61
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 4 MTGSPSSISASVGDRVTTCRTSQTISRILNMYQQIPEKAPKLIIFAASTLTGTGPSRFG 63
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 62 GSGSGTEFTLTISNQEPDFASYCOOSYTLTYTGSGTKLEIKR 106
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 64 GSGSGTDFLTISTLPDPDFATYYCOGSYTTPYTFGGQGTKLEIKR 108
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 12
KHUDE
Ig kappa chain V-I region (Dee) - human (tentative sequence)
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A01865
R:Milstein, C.P.; Deverson, E.V.
Biochem. J. 123, 945-958, 1971.
A>Title: The amino acid sequence of a human kappa light chain.
A:Reference number: A01865; MUID:72053133; PMID:5124396
A:Accession: A01865
A:Molecule type: protein
A:Residues: 1-108 <ML>
A>Note: the C region of this chain as the Inv (3) marker
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Distal disulfide bonds: #status predicted

Query Match      82.1%; Score 449; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 3,1e-34;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTGSPSSISASVGRVTTCRARGISITLYLNWYQKPKAKLIWSASNIGCVPSRF 60
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 3 ZMTGSPSSISASVGRVTTCRAGSVNKTLYNWYQKPKALIFPASSLKSGVPSRF 62
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 61 SSGSGTEFTLTISNQEPDFASYCOOSYTLTYTGSGTKLEIKR 106
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 63 SSGSGTDFLTISTLPDPDFATYYCOGSYTTPYTFGGQTKLEIKR 108
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 13
S19674
Ig kappa chain V region (clone alpha-TEL9) - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19674
R:Markus, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A>Title: By-passing immunization. Human antibodies displayed on V-gene libraries displayed on phage.
A:Reference number: S19663; MUID:92085276; PMID:1746994
A:Accession: S19674
A:Molecule type: mRNA

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A:Residues: 1-108 <MAR>
A:Cross-references: EMBL:X61642; NID:g37860; PIDD:CAA43823.1; PID:g1335386
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 447; DB 2; Length 108;
Best Local Similarity 83.8%; Pred. No. 4,7e-34;
Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY      2 LTGSPSSISASVGDVAVITTCRAQSISTYLNWYQKPKGAPKLLIMSASNLQGVPSRFS 61
DB      4 LTGSPSSISASVGDVAVITTCRAQSISINYLNWYQKPKGAPKLLIYAATLQGVPSRFS 63

QY      62 GSGSGTEFTLTISNLQFEDPASYYCOQSYTTLTTFGSGTLEIKR 106
DB      64 GSGSGTDFTLTINSLOPEDFATYYCOQTSFPLTFGGGTLEIKR 108

RESULT 14
S40317
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40317
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:9408091; PMID:8258341
A:Accession: S40317
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: EMBL:X72427; NID:g441322; PIDD:CAA51095.1; PID:g441323
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match      81.5%; Score 446; DB 2; Length 129;
Best Local Similarity 81.0%; Pred. No. 7e-34;
Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY      1 ELTQSPSSISASVGDVAVITTCRAQSISTYLNWYQKPKGAPKLLIMSASNLQGVPSRF 60
DB      24 QMTQSPSSLSTSLGDRVITTCRAQSISIGTILNWYQKPKGAPKFLIYGASSLQGVPSRF 83

QY      61 GSGSGTEFTLTISNLQFEDPASYYCOQSYTTLTTFGSGTKLEIK 105
DB      84 GSGSGTDFTLTINSLOPEDFATYYCOQTSFPLTFGGGTLEIKR 128

RESULT 15
S46371
Ig kappa chain V-J region (724-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46371; S38645
R:Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination.
A:Reference number: S46369; MUID:9431975; PMID:8039491
A:Accession: S46371
A:Molecule type: mRNA
A:Residues: 1-117 <BNM>
A:Cross-references: EMBL:Z27172; NID:g415959; PIDD:CAA81696.1; PID:g415960
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:23-97/Domain: immunoglobulin homology <IMM>

Query Match      80.1%; Score 438; DB 2; Length 117;
Best Local Similarity 80.6%; Pred. No. 3.4e-33;
Matches 87; Conservative 10; Mismatches 9; Indels 2; Gaps 1;

```

```
Oy      1 ELTOSPPSSIASVGDRTVITTCRAPOSISTYLNMYOQKPGKAPKLLIMSASNLQSGVPSRF 60
      ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      10 QMTOSPSTLSASVGDRTVITTCRAPRSISTWLANWQKPGKAPKLLIKASTLESQVPSRF 69
      ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy      61 SGSSGSGTEFTLTISNLQPEDFASYCQ--SYTTLTYTGGSGTKLEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      70 SGSSGSGTEFTLTISLQPDDFATYCCQYNSYFPPTYFGQTKLEIKR 117
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Search completed: February 10, 2004, 18:41:10  
Job time : 10.9212 secs

**THIS PAGE BLANK (USPTO)**

| Result | No.   | Score | Query Match | Length | DB         | ID     | Description  |
|--------|-------|-------|-------------|--------|------------|--------|--------------|
| 1      | 453   | 82.8  | 129         | 1      | KV1V_HUMAN | P04431 | homo sapiens |
| 2      | 449   | 82.1  | 108         | 1      | KV1E_HUMAN | P01597 | homo sapiens |
| 3      | 437   | 79.9  | 108         | 1      | KV1H_HUMAN | P01600 | homo sapiens |
| 4      | 424   | 77.5  | 108         | 1      | KV1N_HUMAN | P01606 | homo sapiens |
| 5      | 416   | 76.1  | 108         | 1      | KV1O_HUMAN | P01654 | homo sapiens |
| 6      | 416   | 76.1  | 108         | 1      | KV1O_HUMAN | P01607 | homo sapiens |
| 7      | 413.5 | 75.6  | 107         | 1      | KV1D_HUMAN | P01596 | homo sapiens |
| 8      | 412   | 75.3  | 129         | 1      | KV1X_HUMAN | P04432 | homo sapiens |
| 9      | 411.5 | 75.2  | 109         | 1      | KV1T_HUMAN | P01612 | homo sapiens |
| 10     | 411   | 75.1  | 108         | 1      | KV1S_HUMAN | P01611 | homo sapiens |
| 11     | 408   | 74.6  | 108         | 1      | KV1V_HUMAN | P04430 | homo sapiens |
| 12     | 407   | 74.4  | 108         | 1      | KV1E_HUMAN | P01598 | homo sapiens |
| 13     | 403   | 73.7  | 108         | 1      | KV1P_HUMAN | P01608 | homo sapiens |
| 14     | 402   | 73.5  | 108         | 1      | KV1A_HUMAN | P01593 | homo sapiens |
| 15     | 402   | 73.5  | 108         | 1      | KV1G_HUMAN | P01599 | homo sapiens |
| 16     | 401   | 73.3  | 108         | 1      | KV1L_HUMAN | P01604 | homo sapiens |
| 17     | 401   | 73.3  | 108         | 1      | KV1Y_HUMAN | P01602 | homo sapiens |
| 18     | 399   | 72.9  | 108         | 1      | KV1R_HUMAN | P01610 | homo sapiens |
| 19     | 396   | 72.4  | 108         | 1      | KV1C_HUMAN | P01595 | homo sapiens |
| 20     | 395   | 72.2  | 108         | 1      | KV1M_HUMAN | P01605 | homo sapiens |
| 21     | 393   | 71.8  | 108         | 1      | KV1K_HUMAN | P01603 | homo sapiens |
| 22     | 384   | 70.2  | 108         | 1      | KV1Q_HUMAN | P01609 | homo sapiens |
| 23     | 384   | 70.2  | 108         | 1      | KV5M_MOUSE | P01646 | mus musculus |
| 24     | 383   | 70.0  | 117         | 1      | KV1J_HUMAN | P01602 | homo sapiens |
| 25     | 377   | 68.9  | 117         | 1      | KV1I_HUMAN | P01601 | homo sapiens |
| 26     | 375   | 68.6  | 108         | 1      | KV5N_MOUSE | P01647 | mus musculus |
| 27     | 374   | 68.4  | 108         | 1      | KV5K_MOUSE | P01644 | mus musculus |
| 28     | 373   | 68.2  | 108         | 1      | KV5D_MOUSE | P01636 | mus musculus |
| 29     | 372   | 68.0  | 108         | 1      | KV5I_MOUSE | P01645 | mus musculus |
| 30     | 372   | 68.0  | 108         | 1      | KV5L_MOUSE | P01652 | mus musculus |
| 31     | 372   | 68.0  | 114         | 1      | KV4A_HUMAN | P01655 | homo sapiens |
| 32     | 371   | 67.8  | 108         | 1      | KV5O_MOUSE | P01648 | mus musculus |
| 33     | 371   | 67.8  | 111         | 1      | KV3M_MOUSE | P01665 | mus musculus |

|    |       |      |     |   |            |        |              |
|----|-------|------|-----|---|------------|--------|--------------|
| 34 | 370   | 67.6 | 111 | 1 | KV0_MOUSE  | P01667 | mus musculus |
| 35 | 368   | 67.3 | 111 | 1 | KV1_MOUSE  | P01664 | mus musculus |
| 36 | 367   | 67.1 | 108 | 1 | KV5P_MOUSE | P01649 | mus musculus |
| 37 | 366   | 66.9 | 111 | 1 | KV3Q_MOUSE | P01693 | mus musculus |
| 38 | 366   | 66.9 | 149 | 1 | KV5A_MOUSE | P01633 | mus musculus |
| 39 | 365   | 66.7 | 136 | 1 | KV5B_MOUSE | P01634 | mus musculus |
| 40 | 364.5 | 66.6 | 129 | 1 | KV3L_HUMAN | P18135 | homo sapien  |
| 41 | 363   | 66.4 | 108 | 1 | KV5Q_MOUSE | P01650 | mus musculus |
| 42 | 362   | 66.2 | 111 | 1 | KV3H_MOUSE | P01660 | mus musculus |
| 43 | 362   | 66.2 | 111 | 1 | KV3N_MOUSE | P01665 | mus musculus |
| 44 | 362   | 66.2 | 134 | 1 | KV4C_HUMAN | P06314 | homo sapien  |
| 45 | 361   | 66.0 | 108 | 1 | KV5U_MOUSE | P04966 | mus musculus |

## ALIGNMENTS

## RESULT 1

|    |   |           |      |         |
|----|---|-----------|------|---------|
| ID | KV14M HUMAN   | STANDARD; | PRT; | 129 AA. |
| AC | P0431;  |           |      |         |
| DT | 13-AUG-1987 (Rel. 05, Last sequence update)                       |           |      |         |
| DT | 13-AUG-1987 (Rel. 05, Last sequence update)                       |           |      |         |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update)                     |           |      |         |
| DE | IG kappa chain V-I region Walker precursor.                       |           |      |         |
| OS | Homo sapiens (Human)  |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |           |      |         |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.       |           |      |         |
| OX | NCBI_TaxId=9606;  |           |      |         |
| RN | [1]   |           |      |         |
| RP | SEQUENCE FROM N.A.  |           |      |         |

RX MEDLINE=85014148; PubMed=60910049;  
 RA Klobbeck H.G.; Combariza G.; Zachau H.G.;  
 RT "Immunoglobulin genes of the kappa light chain type  
 from two human  
 lymphoid cell lines are closely related".  
 Nucleic Acids Res. 12:6995-7006(1984).  
 RL

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```
CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01983; KIHUWK.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
CW
```

|    |          |     |     |                                  |
|----|----------|-----|-----|----------------------------------|
| FT | SIGNAL   | 1   | 22  | IG KAPPA CHAIN V-I REGION WALKER |
| FT | CHAIN    | 23  | 129 | FRAMEWORK-1.                     |
| FT | DOMAIN   | 23  | 45  | COMPLEMENTAITY-DETERMINING-1.    |
| FT | DOMAIN   | 46  | 56  | COMPLEMENTAITY-DETERMINING-2.    |
| FT | DOMAIN   | 57  | 71  | FRAMEWORK-2.                     |
| FT | DOMAIN   | 72  | 78  | COMPLEMENTAITY-DETERMINING-3.    |
| FT | DOMAIN   | 79  | 110 | FRAMEWORK-4.                     |
| FT | DOMAIN   | 111 | 119 | COMPLEMENTAITY-DETERMINING-3.    |
| FT | DOMAIN   | 120 | 129 | FRAMEWORK-4.                     |
| FT | DISULFID | 45  | 110 | BY STIMILARITY.                  |

| FT                    | NON | TER | 129   | 129                | 129                    |
|-----------------------|-----|-----|-------|--------------------|------------------------|
| SEQ                   | 129 | AA: | 14069 | MM:                | P941FA07DAFC2F9 CRC64: |
| Query Match           |     |     | 82.8% | Score 453:         | DB 1: Length 129       |
| Best Local Similarity |     |     | 83.8% | Pred. No. 1.4e-40: |                        |

Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPKAPKLLIWSASNLQSGVPSRF 60  
 DB 25 QMTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPKAPKLLIWSASNLQSGVPSRF 84

QY 61 SSGSGSTEFLLTISNLOFEDPASVYCOQSYTLLYTFGSGTKLEIK 105  
 DB 85 SSGSGSTEFLLTISNLOFEDPASVYCOQSYTLLYTFGSGTKLEIK 129

RESULT 2  
 KVIH HUMAN STANDARD; PRT; 108 AA.

ID KVIH HUMAN STANDARD; PRT; 108 AA.

AC P01597;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 19 kappa chain V-I region DEE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCB1\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72053133; PubMed=5124396;  
 RA Mjstrein C.P., Deverson E.V.;  
 RT "The amino acid sequence of a human kappa light chain."  
 RL Biochem. J. 123:945-958 (1971).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG\_V.  
 DR SMART; SM00406; IGV\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 82.1%; Score 449; DB 1; Length 108;  
 Best Local Similarity 80.2%; Pred. No. 3e-40;  
 Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPKAPKLLIWSASNLQSGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPKAPKLLIWSASNLQSGVPSRF 62

QY 61 SSGSGSTEFLLTISNLOFEDPASVYCOQSYTLLYTFGSGTKLEIK 106  
 DB 63 SSGSGSTEFLLTISNLOFEDPASVYCOQSYTLLYTFGSGTKLEIK 108

DE 19 kappa chain V-I region Hau.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCB1\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4097974;  
 RA Watanabe S., Hillebrand N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups."  
 RT Hoppe-Sejler's Z. Physiol. Chem. 351:1291-1295 (1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR HSSP; P80362; IWTU.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IGV\_1.  
 DR SMART; SM00406; IGV\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.9%; Score 437; DB 1; Length 108;  
 Best Local Similarity 78.3%; Pred. No. 5.3e-39;  
 Matches 83; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPKAPKLLIWSASNLQSGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPKAPKLLIWSASNLQSGVPSRF 62

QY 61 SSGSGSTEFLLTISNLOFEDPASVYCOQSYTLLYTFGSGTKLEIK 106  
 DB 63 SSGSGSTEFLLTISNLOFEDPASVYCOQSYTLLYTFGSGTKLEIK 108

RESULT 4  
 KVIH HUMAN STANDARD; PRT; 108 AA.

ID KVIH HUMAN STANDARD; PRT; 108 AA.

AC P01606;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 19 kappa chain V-I region OU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCB1\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=70201507; PubMed=5447531;  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;  
 RT "Macroglobulin structure: variable sequence of light and heavy chains."  
 RL Science 169:56-59 (1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.

DR PIR: A01872; KIHOU.  
 DR HSSP: P01607; IREI.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region.  
 FT DOMAIN 1 23. FRAMEWORK-1.  
 FT DOMAIN 24 34. FRAMEWORK-2.  
 FT DOMAIN 35 49. FRAMEWORK-2-DETERMINING-2.  
 FT DOMAIN 50 56. FRAMEWORK-3.  
 FT DOMAIN 57 88. FRAMEWORK-3-DETERMINING-3.  
 FT DOMAIN 89 97. FRAMEWORK-4.  
 FT DOMAIN 98 107. FRAMEWORK-4.  
 FT DISULFID 23 88. BY SIMILARITY.  
 FT NON\_TER 108 108.  
 SQ SEQUENCE 108 AA; 11777 MW; 8283DA42A105827E CRC64;  
 Query Match 77.5%; Score 424; DB 1; Length 108;  
 Best Local Similarity 68.9%; Pred. No. 1,2e-37;  
 Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;  
 Oy 1 ELTQSPSSLSASVGDRTVITTCARQSIITYLNTWYQKPKGKAPKLLIWSASNIQSGVPSRF 60  
 Db 3 QMTZSPSSLSASVGDRTVITTCARQSIITYLNTWYQKPKGKAPKLLIWSASNIQSGVPSRF 62  
 Oy 61 SGGSGGTFTLTISNLQPEDFASYYCOQSYTTLTYPGSGTKLEIKR 106  
 Db 63 SGGSGGTFTLTISNLQPEDFASYYCOQSYTTLTYPGSGTKLEIKR 108  
 RESULT 5  
 KY1B\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01594;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-I region AU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA Schleich H., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 RT protein AU).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=77022433; PubMed=1234024;  
 RA Fehlhauer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
 RA Schwaiger P., Steigemann W., Schramm H.J.;  
 RT "The structure determination of the variable portion of the  
 RT Bence-Jones protein AU";  
 RL Biochem. Struct. Mech. 1:139-146(1975).  
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
 CC REGION OF THE KAPPA CHAIN REI.  
 CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.  
 CC PIR: A91653; KIHOU.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.

DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 FT DOMAIN 1 23. FRAMEWORK-1.  
 FT DOMAIN 24 34. FRAMEWORK-2.  
 FT DOMAIN 35 49. FRAMEWORK-2-DETERMINING-2.  
 FT DOMAIN 50 56. FRAMEWORK-3.  
 FT DOMAIN 57 88. FRAMEWORK-3-DETERMINING-3.  
 FT DOMAIN 89 97. FRAMEWORK-4.  
 FT DOMAIN 98 107. FRAMEWORK-4.  
 FT DISULFID 23 88. BY SIMILARITY.  
 FT NON\_TER 108 108.  
 SQ SEQUENCE 108 AA; 11939 MW; E801187E6F6FB9 CRC64;  
 Query Match 76.1%; Score 416; DB 1; Length 108;  
 Best Local Similarity 76.4%; Pred. No. 8.4e-37;  
 Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;  
 Oy 1 ELTQSPSSLSASVGDRTVITTCARQSIITYLNTWYQKPKGKAPKLLIWSASNIQSGVPSRF 60  
 Db 3 QMTZSPSSLSASVGDRTVITTCARQSIITYLNTWYQKPKGKAPKLLIWSASNIQSGVPSRF 62  
 Oy 61 SGGSGGTFTLTISNLQPEDFASYYCOQSYTTLTYPGSGTKLEIKR 106  
 Db 63 SGGSGGTFTLTISNLQPEDFASYYCOQSYTTLTYPGSGTKLEIKR 108  
 RESULT 6  
 KY1O\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01607;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-I region Rel.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76023758; PubMed=809329;  
 RA Palm W., Hilschmann N.;  
 RT "The primary structure of a crystalline monoclonal immunoglobulin  
 RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation  
 RT and characterization of the tryptic peptides; the complete amino acid  
 RT sequence of the protein; a contribution to the elucidation of the  
 RT three-dimensional structure of antibodies, in particular their  
 RT combining site";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=76039968; PubMed=1182131;  
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;  
 RT "The molecular structure of a dimer composed of the variable portions  
 RT of the Bence-Jones protein REI refined at 2.0-A resolution.";  
 RL Biochemistry 14:4943-4952(1975).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC PIR: A91653; KIHOU.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.





FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 79 110 FRAMEWORK-3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 120 129 FRAMEWORK-4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON TER 129 129  
SQ SEQUENCE 129 AA; 14235 MW; CAF076BCE574C8 CRC64;

Query Match 75.3%; Score 412; DB 1; Length 129;  
Best Local Similarity 74.3%; Pred. No. 2.7e-36;  
Matches 78; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITTCARQSIISTYLMWYQOKGKAPKLLIWSASNLQSGVPSRF 60  
DB 25 QMTQSPSSLSASVGRVITTCARQSIISTYLMWYQOKGKAPKLLIWSASNLQSGVPSRF 84  
QY 61 SGSGSGTEFTLTISNLPEDPASYCCOQSYTTLTYFGSGTKLEIK 105  
DB 85 SGSGSGTEFTLTISNLPEDPASYCCOQSYTTLTYFGSGTKLEIK 129

## RESULT 9

KVLT\_HUMAN STANDARD; PRT; 109 AA.  
ID P01612;  
AC 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ig kappa chain V-I region Mew.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OK NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=83081018; PubMed=6816713;  
RA Bultz M., Linke R.P.;

RT "Primary structure of the variable part of an amyloidogenic  
RT Bence-Jones Protein (Mew). An unusual insertion in the third  
RT hypervariable region of a human kappa-immunoglobulin light chain."  
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358 (1982).  
CC -1- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO  
CC FOUND  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR: A01879; KIHOMV.  
DR HSSP: P80362; 1WTL.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; P:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003596; IG\_MHC.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IGV\_1.  
DR PROSITE: PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.

KM Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 98 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 99 108 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 109 109  
SQ SEQUENCE 109 AA; 11870 MW; B6ABF451SD55F5A0 CRC64;

Query Match 75.2%; Score 411.5; DB 1; Length 109;  
Best Local Similarity 76.6%; Pred. No. 2.5e-36;  
Matches 82; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 ELTOSPSLSASVGRVITTCARQSIISTYLMWYQOKGKAPKLLIWSASNLQSGVPSRF 60  
DB 25 QMTQSPSSLSASVGRVITTCARQSIISTYLMWYQOKGKAPKLLIWSASNLQSGVPSRF 84

DB 3 QMTQSPSSLSASVGRVITTCARQSIISTYLMWYQOKGKAPKLLIWSASNLQSGVPSRF 62

QY 61 SGSGSGTEFTLTISNLPEDPASYCCOQSYTTLTYFGSGTKLEIK 106  
DB 63 SGSGSGTEFTLTISNLPEDPASYCCOQSYTTLTYFGSGTKLEIK 109

## RESULT 10

KVLT\_HUMAN STANDARD; PRT; 108 AA.  
ID P01611;  
AC 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1993 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Mew.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OK NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=81092279; PubMed=6778806;  
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;

RT "Preparative separation of the tryptic hydrolysate of a protein by  
RT high-pressure liquid chromatography. The primary structure of a  
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones protein  
RT Wes)."  
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR: A01877; KIHUMS.  
DR HSSP: P80362; 1WTL.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; P:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003596; IG\_MHC.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IGV\_1.  
DR PROSITE: PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.

KM Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 75.1%; Score 411; DB 1; Length 108;  
Best Local Similarity 74.5%; Pred. No. 2.8e-36;  
Matches 79; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITTCARQSIISTYLMWYQOKGKAPKLLIWSASNLQSGVPSRF 60  
DB 3 QMTQSPSSLSASVGRVITTCARQSIISTYLMWYQOKGKAPKLLIWSASNLQSGVPSRF 62  
QY 61 SGSGSGTEFTLTISNLPEDPASYCCOQSYTTLTYFGSGTKLEIK 106  
DB 63 SGSGSGTEFTLTISNLPEDPASYCCOQSYTTLTYFGSGTKLEIK 108

## RESULT 11

KVLT\_HUMAN STANDARD; PRT; 108 AA.  
ID P04430;  
AC 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1993 (Rel. 38, Last annotation update)

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DE Ig kappa chain V-I region BAN.
OC Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUBN.
DR HSSP; P80362; 1WTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; I:lg-like.
DR InterPro; IPR003006; I: MHC.
DR InterPro; IPR003596; I: V.
DR Pfam; PF00047; I: I.
DR SMART; SM00406; I: I.
DR PROSITE; PS00835; I: I_LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3PD944FE96FD37 CRC64;

Query Match 74.4%; Score 408; DB 1; Length 108;
Best Local Similarity 74.5%; Pred. No. 5.8e-36;
Matches 79; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITTCRAROSISTLYNMYQOKPGKAPKLLIWSASNIQGVPSRF 60
DB 3 QLTQSPSSLSASVGDRTITTCRASQSYNYNVAFOQPGKAPSLIYDASTLOSQVPSNF 62
QY 61 SSGSGTEFTLTISNLOFEDFASYYCCQSYTYLTFGSGTKLEIKR 106
DB 63 TSGSGTDFITLTISLQPDPAFYTCQYNSPYTTEGQTKVQIKR 108

RESULT 12
KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01558;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gali W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).

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CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A90562; KIHBU.
DR HSSP; P01607; IREL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; I:lg-like.
DR InterPro; IPR003006; I: MHC.
DR InterPro; IPR003596; I: V.
DR Pfam; PF00047; I: I.
DR SMART; SM00406; I: I.
DR PROSITE; PS00835; I: I_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 74.4%; Score 407; DB 1; Length 108;
Best Local Similarity 74.3%; Pred. No. 7.3e-36;
Matches 78; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITTCRAROSISTLYNMYQOKPGKAPKLLIWSASNIQGVPSRF 60
DB 3 QLTQSPSSLSASVGDRTITTCRASQSYNYNVAFOQPGKAPKLLIWSASNIQGVPSNF 62
QY 61 SSGSGTEFTLTISNLOFEDFASYYCCQSYTYLTFGSGTKLEIKR 105
DB 63 ISSGSGTEFTLTISLQPDPAFYTCQYNSDKMGQSTKVEK 107

RESULT 13
KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region ROY.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponetling H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
RL -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A91638; KIHURY.
DR HSSP; P80362; 1WTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; I:lg-like.

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DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match
Best Local Similarity 73.7%; Score 403; DB 1; Length 108;
Matches 77; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPKAKLLIWSASNLQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPKAKLLIWSASNLQGVPSRF 62
QY 61 SGSGSGTEFTLTISNLOPEDPASYYCOQSYTTLTYFGSGTLEIKR 106
DB 63 SGSGGTEFTLTISNLOPEDPASYYCOQSYTTLTYFGSGTLEIKR 108

RESULT 14
KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969). THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR: A01861; KIHUNG.
DR HSSP: P01607; IREI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

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Query Match
Best Local Similarity 73.5%; Score 402; DB 1; Length 108;
Matches 79; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPKAKLLIWSASNLQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPKAKLLIWSASNLQGVPSRF 62
QY 61 SGSGSGTEFTLTISNLOPEDPASYYCOQSYTTLTYFGSGTLEIKR 106
DB 63 SGSGGTEFTLTISNLOPEDPASYYCOQSYTTLTYFGSGTLEIKR 108

RESULT 15
KV1G_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC PIR: A01867; KIHUGL.
DR HSSP: P01607; IREI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match
Best Local Similarity 73.5%; Score 402; DB 1; Length 108;
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPKAKLLIWSASNLQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPKAKLLIWSASNLQGVPSRF 62
QY 61 SGSGSGTEFTLTISNLOPEDPASYYCOQSYTTLTYFGSGTLEIKR 106
DB 63 SGSGGTEFTLTISNLOPEDPASYYCOQSYTTLTYFGSGTLEIKR 108

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Wed Feb 11 06:06:09 2004

us-10-027-725a-11.rsp

Search completed: February 10, 2004, 18:36:31  
Job time : 5.94242 secs

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Db 3 QMTQSPSSLSASVGDRTVITTCRASQISISYLNWYQKPKAPNLIYAASLSQGVPSRF 62  
 QY 61 SSGSGSTEFTLTISNLOFEDFASYYCOOSYTTLYTFSGTKLEIKR 106  
 DB 63 SSGSGSTDFTLTISLQPEDFATYYCOOSYSTSWTFEGTKVEIKR 108

## RESULT 2

Q96SA9 PRELIMINARY; PRT; 107 AA.

AC Q96SA9; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes";  
 RL J. Immunol. 161:2020-2031(1998).  
 DR EMBL; U96396; AAB68785.1; -  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 85.1%; Score 465.5; DB 4; Length 107;  
 Best Local Similarity 85.8%; Pred. No. 2.4e-44;  
 Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISISYLNWYQKPKAPNLIYAASLSQGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDRTVITTCRASQISISYLNWYQKPKAPNLIYAASLSQGVPSRF 62  
 QY 61 SSGSGSTEFTLTISNLOFEDFASYYCOOSYTTLYTFSGTKLEIKR 106  
 DB 63 SSGSGSTDFTLTISLQPEDFATYYCOOSYSTL-TFEGTKVEIKR 107

## RESULT 3

Q9UL81 PRELIMINARY; PRT; 107 AA.

AC Q9UL81; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035033; AAD56269.1; -  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 82.0%; Score 448.5; DB 4; Length 107;  
 Best Local Similarity 82.1%; Pred. No. 1.9e-42;  
 Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISISYLNWYQKPKAPNLIYAASLSQGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDRTVITTCRASQISISYLNWYQKPKAPNLIYAASLSQGVPSRF 62  
 QY 61 SSGSGSTEFTLTISNLOFEDFASYYCOOSYTTLYTFSGTKLEIKR 106  
 DB 63 SSGSGSTDFTLTISLQPEDFATYYCOOSYSTL-TFEGTKVEIKR 107

## RESULT 4

Q9UL70 PRELIMINARY; PRT; 108 AA.

AC Q9UL70; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035044; AAD56280.1; -  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 75.7%; Score 414; DB 4; Length 108;  
 Best Local Similarity 77.4%; Pred. No. 1.4e-38;  
 Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISISYLNWYQKPKAPNLIYAASLSQGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDRTVITTCRASQISISYLNWYQKPKAPNLIYAASLSQGVPSRF 62  
 QY 61 SSGSGSTEFTLTISNLOFEDFASYYCOOSYTTLYTFSGTKLEIKR 106  
 DB 63 SSGSGSTDFTLTISLQPEDFATYYCOOSYSTL-TFEGTKVEIKR 108

## RESULT 5

Q9UL79

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ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98377139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSBP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT TER 108
SQ SEQUENCE 108 AA; 1187 MW; DB5845F19724FB4E CRC64;

Query Match 75.5%; Score 413; DB 4; Length 108;
Best Local Similarity 77.1%; Pred. No. 1.8e-38;
Matches 81; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRARQSTSTYLNWYQOKRGPAPKLLIWSASNLQGVPSRF 61
DB 4 MTQSPSLASLSTGDRVITSCRAQDLSNINWYQOKRGPAPKLLIWSASNLQGVPSRF 63
QY 62 GSGSGTEFTLTISNLQFEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
DB 64 GSGSGTDFLTISLQSGEDFATYYCQYYSPPTFGGKTKLEIKR 108

RESULT 6
Q9QYFO PRELIMINARY; PRT; 298 AA.
ID Q9QYFO;
AC Q9QYFO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CN 8 scFv.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c; Tissue=Spleen;
RX MEDLINE=20183931; PubMed=10706631;
RA Shiohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA88633.1; -.
DR HSBP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 2.

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DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 3167 MW; E0F968BA17004317 CRC64;

Query Match 70.7%; Score 387; DB 11; Length 298;
Best Local Similarity 69.8%; Pred. No. 5.1e-35;
Matches 74; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQSTSTYLNWYQOKRGPAPKLLIWSASNLQGVPSRF 60
DB 175 ELTQSPSLASLSTGDRVITSCRAQDLSNINWYQOKRGPAPKLLIWSASNLQGVPSRF 234
QY 61 GSGSGTEFTLTISNLQFEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
DB 225 GSGSGTGYSLKINSLOPEDFGSYCQHFMTTPTFGGKTKLEIKR 280

RESULT 7
Q91WF8 PRELIMINARY; PRT; 234 AA.
ID Q91WF8;
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=Colon;
RA Strusberg R.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B06EB7812D2 CRC64;

Query Match 69.3%; Score 379; DB 11; Length 234;
Best Local Similarity 68.9%; Pred. No. 2.9e-34;
Matches 73; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQSTSTYLNWYQOKRGPAPKLLIWSASNLQGVPSRF 60
DB 23 QMTQTSLSASLSTGDRVITSCRAQDLSNINWYQOKRGPAPKLLIWSASNLQGVPSRF 82
QY 61 GSGSGTEFTLTISNLQFEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
DB 83 GSGSGTGYSLKINSLOPEDFGSYCQHFMTTPTFGGKTKLEIKR 128

RESULT 8
Q96PF6 PRELIMINARY; PRT; 116 AA.
ID Q96PF6;
AC Q96PF6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;

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RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;  
RT "the tropism of organ involvement in primary systemic amyloidosis:  
RT contributions of Ig V(L) germ line gene use and clonal plasma cell  
RT burden."

RL Blood 98:714-720 (2001).  
DR EMBL; AF361758; AAK51465.1; -  
DR InterPro; IPR007110; IG\_1ike.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1 1  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BRCF57 CRC64;

Query Match 68.4%; Score 374; DB 4; Length 116;  
Best Local Similarity 66.0%; Pred. No. 4.4e-34;  
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTTTCRARSISTYLNWYQKQKAPKLLMSASNLQSGVPSRF 60  
DB 3 QMTQSPSLASASVGDRTTTCRARSISTYLNWYQKQKAPKLLMSASNLQSGVPSRF 62  
QY 61 SSGSGSTEFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
DB 63 SSGSGSATNFTVTITSLQPEDFATYYCOQYHLPFTGPGTKVDPKR 108

RESULT 9  
Q8R062 PRELIMINARY; PRT; 234 AA.

ID Q8R062  
AC Q8R062;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical 25.9 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC027418; AAK27418.1; -  
DR InterPro; IPR007110; IG\_1ike.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
DR PROSITE; PSS0290; IG\_MHC; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEB1 CRC64;

Query Match 68.4%; Score 374; DB 11; Length 234;  
Best Local Similarity 69.8%; Pred. No. 1.1e-33;  
Matches 74; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTTTCRARSISTYLNWYQKQKAPKLLMSASNLQSGVPSRF 60  
DB 23 QMTQSPSLASASVGDRTTTCRARSISTYLNWYQKQKAPKLLMSASNLQSGVPSRF 82  
QY 61 SSGSGSTEFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
DB 83 SSGSGSTHYSGLTISNLEPDIAIYYCQYSGPFTTSGTKLEIKR 128

RESULT 10  
Q920E6 PRELIMINARY; PRT; 109 AA.

AC Q920E6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Pterin-mimicking anti-idiotope kappa chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaltie O., Cotton R.G.H.;  
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed  
RT in Mammalian Cells." to the EMBL/GenBank/DBJ databases.  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307938; AAL09422.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1 1  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;

Query Match 68.2%; Score 373; DB 11; Length 109;  
Best Local Similarity 66.0%; Pred. No. 5.3e-34;  
Matches 70; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTTTCRARSISTYLNWYQKQKAPKLLMSASNLQSGVPSRF 60  
DB 3 QMTQSPSLASASVGDRTTTCRARSISTYLNWYQKQKAPKLLMSASNLQSGVPSRF 62  
QY 61 SSGSGSTEFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
DB 63 SSGSGSTYSLKINSNLQPEDFSGYCOHFWSTPMTFGGTKLEIKR 108

RESULT 11

ID Q9UL83  
AC Q9UL83;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL; AF035031; AAD56267.1; -  
DR HSP; P80362; IWT.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1 1  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;



|                       |        |                    |                |             |
|-----------------------|--------|--------------------|----------------|-------------|
| Query Match           | 67.8%; | Score 371;         | DB 4;          | Length 108; |
| Best Local Similarity | 65.7%; | Pred. No. 8.8e-34; |                |             |
| Matches               | 69;    | Conservative 18;   | Mismatches 18; | Indels 0;   |
|                       |        |                    |                | Gaps 0      |

[illegible]

## RESULT 12

ID Q9R1A5 PRELIMINARY; PRT; 214 AA.

|    |   |
|----|---|
| AC | GQR15;  |
| DT | 01-MAY-2000 (T-EMBLrel. 13, Created)  |
| DT | 01-MAY-2000 (TEMBRel. 13, Last sequence update)   |
| DE | 01-MAR-2003 (TEMBlrel. 23, Last annotation update)  |
| DE | Kappa light chain of Mab7 (fragment).   |
| OS | Mus musculus (Mouse).   |
| OC | Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |
| OX | NBI_TaxID=10090;  |
| RN | [1]   |
| RP | SEQUENCE FROM N.A.<br>Wildie K.G., Yu X., Ekramodoullah A.K.M., Misra S.;<br>RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal<br>antibody (Mab 7 , its light and heavy chains) and construction of a<br>single chain antibody (scFv).";<br>RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.<br>DR EMBL; AF152371; RAND40242.1; -.<br>HSSP; P01679; 2PBUT.<br>DR InterPro; IPR007110; Ig-like.<br>DR InterPro; IPR003008; IG_MHC.<br>DR InterPro; IPR003596; Ig_v.<br>pfam; PF00047; ig_2.<br>SMART; SM00406; IGV; 1.<br>DR PROSITE; PSS0835; IG_LIKE; 2.<br>DR PROSITE; PSS0290; IG_MHC; 1.<br>FT NON_TER 1<br>PT NON_TER 1 |
| SQ | SEQUENCE 214 AA; 23922 MW; 52BA205FD895SE2A CRC64;  |

|                       |        |                    |                |             |
|-----------------------|--------|--------------------|----------------|-------------|
| Query Match           | 67.3%; | Score 368;         | DB 11;         | Length 214; |
| Best Local Similarity | 65.1%; | Pred. No. 4.5e-33; |                |             |
| Matches               | 69;    | Conservative 19;   | Mismatches 18; | Indels 0;   |
|                       |        |                    |                | Gaps 0      |

[illegible]

## RESULT 13

|    |        |              |      |     |    |
|----|--------|--------------|------|-----|----|
| ID | Q8VCP0 | PRELIMINARY; | PRT; | 234 | AA |
|----|--------|--------------|------|-----|----|

DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical 25.7 kDa protein.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
OX NCBI\_taxid=10090;  
RN (1)  
RP  
RC  
SEQUENCE FROM N.A.  
TISSUE=Colon;

RA Strausberg R.;  
 Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases

DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

[illegible]

## RESULT 14

|    |        |              |      |        |
|----|--------|--------------|------|--------|
| ID | Q920E9 | PRELIMINARY; | PRT; | 111 AA |
|----|--------|--------------|------|--------|

|    |   |   |
|----|---|---|
| PT | 01-DEC-2001   | (TREMBLrel. 19, Created)                |
| DT | 01-DEC-2001   | (TREMBLrel. 19, Last sequence update)   |
| DT | 01-MAR-2003   | (TREMBLrel. 23, Last annotation update) |
| DE | Pterin-mimicking anti-idiotope kappa chain variable region<br>(fragment). |   |
| OC | Mus musculus (Mouse).   |   |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;         |   |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.        |   |
| OX | NBCL_TaxID=10090;   |   |
| RN | [1]   |   |
| RP | SEQUENCE FROM N.A.  |   |
| RA | Akin J.D., Iape A., Jennings I.G., Horatis O., Cotton R.G.H.;             |   |
| RT | "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed      |   |
| RL | In Mammalian Cells."  |   |
| RL | Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.                   |   |
| DR | EMBL; AF307935; AAL09419.1; -   |   |
| DR | InterPro; IPRO07110; IG_1like.  |   |
| DR | InterPro; IPRO03006; IG_MHC.  |   |
| DR | InterPro; IPRO03596; IG_V.  |   |
| DR | Plan; PF00047; Ig; 1.   |   |
| DR | SMART; SMO0406; IGV; 1.   |   |
| DR | PROSITE; PSS0835; IG_LIKE; 1.   |   |
| FT | NON_TER   |   |
| FT | NON_TER   |   |
| Q  | SEQUENCE  |   |
|    | 111 AA; 12046 MW; 1E46588AA6858526 CRC64;                                 |   |

|                       |        |                    |        |                |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match           | 66.9%; | Score 366;         | DB 11; | Length 111;    |
| Best Local Similarity | 65.7%; | Pred. No. 3.3e-33; |        |                |
| Matches               | 71;    | Conservative       | 16;    | Mismatches 17; |
|                       |        |                    | Indels | 4;             |
|                       |        |                    | Gaps   | 1;             |

```

OY      LTSPSPSLASVSDRVTITICRAQSIST----YLYNYYQQRKPGAPKLLITWMSNLSQGV 5
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4 LTSPSPSLANVSLQGRATISCRASKSVSTSGYSIMHMYQQKPGQPKLLIYIASNLSQGV 6
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY      58 SRSSGSGSGTEFPTLITSLNLFQEDFPASYYCQOSTTLLITGSGCKLEIK 105
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      64 ARSSGSGSGTDFPTLINTHPEEEDAAAYYYCHSKELDYTPGGGCKLEIK 111
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 15

|    |        |              |      |     |    |
|----|--------|--------------|------|-----|----|
| ID | Q91WS9 | PRELIMINARY; | PRT; | 233 | AA |
|----|--------|--------------|------|-----|----|

|    |   |
|----|---|
| DT | 01-DEC-2001 (TremblRel. 19, Created)              |
| DT | 01-DEC-2001 (TremblRel. 19, Last sequence update) |

```

DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AH13496.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 66.5%; Score 364; DB 11; Length 233;
Best Local Similarity 67.0%; Pred. No. 1,4e-32;
Matches 71; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITTCRARQSTISTYLNWYQKPGKAPKLLIWSASNLQGVPSRF 60
   :||:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 22 QMTQTTSLSASLGDRTVISCSSQGIANYLNWYQKPDGTVKLLIYTTSSLHSGVPSRF 81
   :||:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:

QY 61 SSGSGGTEFTLTISNLFEDPASVYCCQSYTTLTFSGGKLEIKR 106
   |||||:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 82 SSGSGGTDYSLTISNLEPDIAITYCCQRYRLPMTFGGKLEIKR 127
   |||||:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:

```

Search completed: February 10, 2004, 18:39:23  
 Job time : 26.0545 secs

|  |    |       |      |     |    |           |                     |
|--|----|-------|------|-----|----|-----------|---------------------|
|  | 10 | 476   | 87.0 | 107 | 21 | AAV982136 | Anti-gp120 antibody |
|  | 11 | 476   | 87.0 | 107 | 21 | AAV982136 | Anti-gp120 antibody |
|  | 12 | 475   | 86.8 | 107 | 22 | AAG93663  | Human anti-Rh(D) a  |
|  | 13 | 475   | 86.8 | 107 | 22 | AAG93664  | Human anti-Rh(D) a  |
|  | 14 | 474   | 86.7 | 107 | 22 | AAG93667  | Human anti-Rh(D) a  |
|  | 15 | 473.5 | 86.6 | 108 | 22 | AAAG93589 | Human anti-Rh(D) c  |
|  | 16 | 473.5 | 86.6 | 108 | 22 | AAAG93600 | Human anti-Rh(D) c  |
|  | 17 | 473   | 86.5 | 107 | 22 | AAAG93594 | Human anti-Rh(D) c  |
|  | 18 | 473   | 86.5 | 111 | 22 | AAAG63656 | Amino acid sequenc  |
|  | 19 | 473   | 86.5 | 111 | 24 | ABJ38615  | Hepatitis C virus   |
|  | 20 | 473   | 86.5 | 240 | 24 | ABJ38595  | Hepatitis C virus   |
|  | 21 | 473   | 86.5 | 299 | 22 | AAAG63660 | Hepatitis C virus   |
|  | 22 | 472.5 | 86.4 | 108 | 22 | AAAG93655 | Amino acid sequenc  |
|  | 23 | 472.5 | 86.3 | 107 | 22 | AAAG93595 | Human anti-Rh(D) c  |
|  | 24 | 472   | 86.3 | 107 | 22 | AAAG93596 | Human anti-Rh(D) c  |
|  | 25 | 472   | 86.3 | 107 | 22 | AAAG93650 | Human anti-Rh(D) a  |
|  | 26 | 471   | 86.1 | 107 | 22 | AAAG93646 | Human anti-Rh(D) a  |
|  | 27 | 470   | 85.9 | 108 | 24 | AAO16704  | Human anti-blood c  |
|  | 28 | 470   | 85.9 | 108 | 24 | AAO16705  | Human anti-blood c  |
|  | 29 | 470   | 85.9 | 114 | 18 | AAAI3922  | Light chain #1 fo   |
|  | 30 | 469   | 85.7 | 107 | 22 | AAAG93601 | Human anti-Rh(D) c  |
|  | 31 | 468   | 85.6 | 111 | 22 | AAAG63655 | Amino acid sequenc  |
|  | 32 | 468   | 85.6 | 111 | 24 | ABJ38614  | Hepatitis C virus   |
|  | 33 | 468   | 85.6 | 132 | 18 | AAW28642  | Human anti-tumour   |
|  | 34 | 468   | 85.6 | 240 | 24 | ABJ38594  | Hepatitis C virus   |
|  | 35 | 468   | 85.6 | 299 | 22 | AAAG63659 | Amino acid sequenc  |
|  | 36 | 467   | 85.4 | 108 | 24 | AAE35210  | Human IgE scFv IC2  |
|  | 37 | 467   | 85.4 | 108 | 24 | ABP96009  | HSA antibody relat  |
|  | 38 | 467   | 85.4 | 240 | 20 | AAV02472  | A single chain ant  |
|  | 39 | 467   | 85.4 | 240 | 22 | AAAB46005 | Human MUC-1 scFv c  |
|  | 40 | 467   | 85.4 | 240 | 22 | AAAB46006 | Human MUC-1 scFv c  |
|  | 41 | 467   | 85.4 | 240 | 22 | AAAB46007 | Human MUC-1 scFv c  |
|  | 42 | 467   | 85.4 | 240 | 22 | AAAB46008 | Human MUC-1 scFv c  |
|  | 43 | 467   | 85.4 | 240 | 22 | AAAB46038 | Human Tf anti-idio  |
|  | 44 | 467   | 85.4 | 240 | 24 | ABP95997  | Human serum albumin |
|  | 45 | 466   | 85.2 | 114 | 22 | AAG65563  | Amino acid sequenc  |

ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| ABG30449 |   |
| ID       | ABG30449 standard; Protein; 106 AA.                       |
| XX       |   |
| AC       | ABG30449;   |
| XX       |   |
| DT       | 21-OCT-2002 (first entry)                                 |
| XX       |   |
| DE       | Human IgE Fab clone 60 light chain protein.               |
| XX       |   |
| KM       | Human; fab; antiallergic; vaccine; grass pollen; Phi p 2; |
| KW       | timochy grass pollen allergen; passive immunotherapy.     |
| XX       |   |
| OS       | Homo sapiens.   |
| XX       |   |
| FH       | Key   |
| FT       | Region  |
| FT       | /note= "FR1 region"                                       |
| FT       | Region  |
| FT       | /note= "CDR1 region"                                      |
| FT       | Region  |
| FT       | /note= "FR2 region"                                       |
| FT       | Region  |
| FT       | /note= "CDR2 protein"                                     |
| FT       | Region  |
| FT       | /note= "FR3 region"                                       |
| FT       | Region  |
| FT       | /note= "CDR2 region"                                      |
| FT       | Region  |
| FT       | /note= "FR4 region"                                       |
| FT       | Misc-difference 98  |
| FT       | /note= "Encoded by CCT"                                   |

XX WO200253595-A1.  
PN 11-JUL-2002.  
XX 27-DEC-2001; 2001WO-SE02908.  
XX 29-DEC-2000; 2000SE-0004892.  
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.  
XX Flicker S, Steinberger P, Kraft D, Valenta R;  
XX WPI: 2002-583604/62.  
XX N-PSDB; ABR99641.  
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for  
PT environmental allergen detection -  
XX disclosure; Page 40; 45pp; English.  
XX This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergic patients  
CC IgE antibodies to Phl p 2 (a major timothy grass pollen allergen).  
CC The group 2 allergen-specific Fabs of the invention may be useful for  
CC environmental allergen detection and for standardisation of allergen  
CC extracts. The Fabs - or a vaccine against a type I allergy is useful for  
CC passive immunotherapy of type I allergy. It is also useful for  
CC diagnosing a type I allergy. The allergen-specific Fabs of the invention  
CC are useful for inner alle, diagnosis, therapy and prevention of type  
CC I allergy. They are also useful for identification of group 2  
CC allergen-containing pollen and may be used for blocking the binding of  
CC grass pollen allergic patients and IgE antibodies to Phl p 2. The present  
CC sequence represents the human IgG fab, clone 60 light chain protein of  
CC the invention.  
XX SQ Sequence 106 AA;  
XX Query Match 98.2%; Score 537; DB 23; Length 106;  
XX Best local Similarity 99.1%; Pred. No. 2.4e-30;  
XX Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDRTITTCARQGISITVLMWYQKPKGAPKLLIWSASNLQSGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTITTCARQGISITVLMWYQKPKGAPKLLIWSASNLQSGVPSRF 60  
QY 61 SGGSGTEFTLTISNLQFEDFASYCQOSYTTLYTGSGTKLEIKR 106  
DB 61 SGGSGTEFTLTISNLQFEDFASYCQOSYTTLYTGSGTKLEIKR 106  
RESULT 2  
AAR54260  
ID AAR54260 standard; protein; 107 AA.  
XX AAR54260;  
XX 25-MAR-2003 (updated)  
DT 10-NOV-1994 (first entry)  
XX Anti-HIV gp120 immunoglobulin light chain variable region b22.  
XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
KM neutralisation; monoclonal antibody; kappa light chain;  
KM variable region; framework; complementarity determining region.  
OS Homo sapiens.  
XX Key Location/Qualifiers

FT Region 1..21  
FT /label= FR1  
FT 22..33  
FT /label= CDR1  
FT Region 34..48  
FT /label= FR2  
FT 49..55  
FT /label= CDR2  
FT Region 56..87  
FT /label= FR3  
FT 88..95  
FT /label= CDR3  
FT 96..107  
FT /label= FR4  
XX WO9407922-A1.  
XX 14-APR-1994.  
XX 30-SEP-1993; 93WO-US09328.  
XX 30-SEP-1992; 92US-0954148.  
XX (SCRI ) SCRIPPS RES INST.  
XX Barbas CF, Burton DR, Lerner RA;  
XX WPI; 1994-135516/16.  
XX New human monoclonal antibodies neutralising HIV - react with  
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo  
PT or in vitro diagnosis and for passive immuno-therapy  
XX Claim 5; Page 189; 248pp; English.  
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR  
CC amplification using primers specific for heavy and light chain  
CC variable regions. The amplification products were inserted into a  
CC diectronic vector to produce a library of fragments. E.coli XL1  
CC blue cells were transformed with the library. Filamentous phage were  
CC produced which expressed the Mab regions on their surface. Panning  
CC with gp120 and gp41 resulted in the recovery of immunoreactive  
CC clones. The light chain VK region sequence AAR54260 neutralises HIV1  
CC gp120.  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 107 AA;  
XX Query Match 88.5%; Score 484; DB 15; Length 107;  
XX Best local Similarity 88.7%; Pred. No. 1.1e-26;  
XX Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDRTITTCARQGISITVLMWYQKPKGAPKLLIWSASNLQSGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTITTCARQGISITVLMWYQKPKGAPKLLIWSASNLQSGVPSRF 60  
QY 61 SGGSGTEFTLTISNLQFEDFASYCQOSYTTLYTGSGTKLEIKR 106  
DB 61 SGGSGTEFTLTISNLQFEDFASYCQOSYTTLYTGSGTKLEIKR 106  
RESULT 3  
AAW01283  
ID AAW01283 standard; Protein; 107 AA.  
XX AAW01283;  
XX 29-JAN-1997 (first entry)  
XX VL region of HIV neutralising Mab, clone b22 and B35.  
XX Heavy chain; light chain; variable region; VH; monoclonal antibody;  
KM Mab; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;

KM virus infectivity assay; precursor gp160; immunocompetence; human;  
 XX anti-HIV antibody; detection; HIV infection.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 XX FT Region 1..21  
 FT Region /label= FR1  
 FT Region 22..32  
 FT Region /label= CDR1  
 FT Region 33..47  
 FT Region /label= FR2  
 FT Region 48..54  
 FT Region /label= CDR2  
 FT Region 55..86  
 FT Region /label= FR3  
 FT Region 87..95  
 FT Region /label= CDR3  
 FT Region 96..107  
 FT Region /label= FR4  
 XX W09602273-A1.  
 XX 01-FEB-1996.  
 XX 11-JUL-1995; 95MO-US08743.  
 XX 18-JUL-1994; 94US-0276852.  
 XX (SCRI ) SCRIPPS RES INST.  
 XX PA  
 XX (SCRI ) SCRIPPS RES INST.  
 XX PI Barbas CF, Burton DR, Lerner RA;  
 XX DR WPI; 1996-179601/18.  
 XX Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in  
 PT passive immuno:therapy and detection of HIV infection.  
 PS Example; Fig 11; 366pp; English.  
 XX The sequences given in AAW01261-92 represent the light chain variable  
 CC regions (VL) of a series of monoclonal antibodies (Mab's) which are  
 CC immunoreactive with HIV glycoprotein gp120 and are capable of  
 CC neutralising HIV. This sequence represents the sequence of the JK2  
 CC gene clones, b22 and B35. A Mab containing this VL sequence has the  
 CC capacity to reduce HIV infectivity titre in an in vivo virus  
 CC infectivity assay by 50 % at a concentration of less than 700 ng  
 CC of antibody/ml, and binds mature gp120 preferentially over the  
 CC precursor gp160. The Mab may be used for determining immunocompetence  
 CC of a human anti-HIV antibody and in the detection of HIV infection.  
 XX SQ Sequence 107 AA;  
 XX Query Match 88.5%; Score 484; DB 17; Length 107;  
 XX Best Local Similarity 88.7%; Pred. No. 1.1e-26;  
 XX Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITTCARQOSISTYLNWYQOKGKAPKLLIWSASNLQGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITTCARQOSISTYLNWYQOKGKAPKLLIWSASNLQGVPSRF 60  
 QY 61 SSGSGGTEFTLTISNLQFEDPASYYCOOSYTTLYTFGSGTKLEIKR 106  
 DB 61 SSGSGGTEFTLTISNLQFEDPASYYCOOSYTTLYTFGSGTKLEIKR 106  
 RESULT 4  
 ID AAY95135 standard; Protein; 107 AA.  
 XX AAY95135;  
 XX 30-JUN-2000 (first entry)

XX Anti-gp120 antibody light chain variable region from clone b22.  
 DE  
 XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;  
 KM reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;  
 KM glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.  
 OS Homo sapiens.  
 XX AU9948756-A.  
 XX 17-FEB-2000.  
 XX 16-SEP-1999; 99AU-0048756.  
 XX 16-SEP-1999; 99AU-0048756.  
 XX (SCRI ) SCRIPPS RES INST.  
 XX PA  
 XX (SCRI ) SCRIPPS RES INST.  
 XX PI Burton DR, Barbas CF, Lerner RA;  
 XX DR WPI; 2000-293393/26.  
 XX Novel human monoclonal antibodies which immunoreact with and neutralise  
 PT human immunodeficiency virus useful for treating HIV infections -  
 XX Example 9; Figure 11; 366pp; English.  
 XX The present sequence represents a fragment of an anti-human  
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV  
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an  
 CC in vitro virus infectivity assay by 50%, at a concentration of less than  
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and  
 CC immunotherapy of HIV induced disease. They are useful as neutralising  
 CC field isolates and provide useful information regarding the  
 CC immunocompetence of an immune response in HIV infected patients. The  
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies  
 CC which can be used to screen human monoclonal antibodies to identify  
 CC whether the antibody has the same binding specificity as the antibodies  
 CC of the invention. The neutralising antibodies define new epitopes on the  
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new  
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the  
 CC monoclonal antibodies derives from the fact that they are encoded by a  
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal  
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly  
 CC reduces the problems of significant host immune response to the passively  
 CC administered antibodies which is a problem commonly encountered when  
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.  
 CC An additional major advantage of the monoclonal antibodies described  
 CC derives from the fact that they immunoreact with a unique determinant  
 CC present on mature HIV glycoprotein gp120. This class of antibodies is  
 CC particularly effective at neutralising field isolates of HIV.  
 XX SQ Sequence 107 AA;  
 XX Query Match 88.5%; Score 484; DB 21; Length 107;  
 XX Best Local Similarity 88.7%; Pred. No. 1.1e-26;  
 XX Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITTCARQOSISTYLNWYQOKGKAPKLLIWSASNLQGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITTCARQOSISTYLNWYQOKGKAPKLLIWSASNLQGVPSRF 60  
 QY 61 SSGSGGTEFTLTISNLQFEDPASYYCOOSYTTLYTFGSGTKLEIKR 106  
 DB 61 SSGSGGTEFTLTISNLQFEDPASYYCOOSYTTLYTFGSGTKLEIKR 106  
 RESULT 5  
 ID AAY98244 standard; Protein; 107 AA.  
 XX AAY98244

XX AAY98244;  
 AC 04-JUL-2000 (first entry)  
 DT  
 DE Anti-gp120 antibody light chain variable region from clone b22.  
 XX  
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;  
 KM human immunodeficiency virus type 1; HIV-1; infectivity titre;  
 KM passive immunotherapy; reduce severity; HIV-induced disease;  
 KM immunocompetence; active immunisation.  
 OS Homo sapiens.  
 XX  
 XX AU9948754-A.  
 PN 17-FEB-2000.  
 PD  
 XX 16-SEP-1999; 99AU-0048754.  
 PF  
 XX 16-SEP-1999; 99AU-0048754.  
 PR  
 XX (SCRI ) SCRIPPS RES INST.  
 PA  
 XX Burton DR, Barbas CF, Lerner RA;  
 PI WPI; 2000-246867/22.  
 DR  
 XX Human neutralizing monoclonal antibodies to human immunodeficiency  
 PT virus (HIV) used for providing passive immunotherapy to HIV are  
 PT specific for glycoprotein-120 -  
 XX  
 XX Example 9; Figure 11; 374pp; English.  
 PS  
 XX This sequence represents a fragment of the antibodies of the invention.  
 CC The invention relates to the production of an anti-HIV (human  
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody  
 CC capable of reducing an HIV infectivity titre in an in vitro virus  
 CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The  
 CC method for the production of the antibody comprises:  
 CC (a) providing a first polynucleotide encoding a heavy chain  
 CC immunoglobulin amino acid sequence (which does not comprise the sequence  
 CC represented by AAY98206) and a second polynucleotide encoding a light  
 CC chain immunoglobulin amino acid sequence;  
 CC (b) inserting the first and second polynucleotide sequences into a host  
 CC cell;  
 CC (c) maintaining the host cell in conditions which allow the amino acid  
 CC sequences encoded by the polynucleotides to be expressed in the host  
 CC cell; and  
 CC (d) isolating the antibody comprising the heavy and light chain  
 CC immunoglobulin amino acid sequences from the host cell.  
 CC The anti-HIV gp-120 monoclonal antibody is used for providing passive  
 CC immunotherapy to HIV in a human. They can be administered to high-risk  
 CC patients to reduce the likelihood and/or severity of HIV-induced disease  
 CC and to patients who are already HIV-infected. The antibodies are used  
 CC for neutralising field isolates which provides information about the  
 CC immunocompetence of an immune response in HIV patients, for detecting  
 CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
 CC producing anti-idiotypic antibodies which can be used for active  
 CC immunisation and to screen human monoclonal antibodies to identify those  
 CC with the same binding specificity and to monitor the course of HIV  
 CC disease therapy by measuring the changes in concentration of HIV present  
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120  
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and  
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
 CC reduce the problems of significant host immune response to the  
 CC antibodies associated with monoclonal antibodies of xenogeneic or  
 CC chimeric derivation.  
 CC  
 XX Sequence 107 AA;  
 SQ

Query Match 88.5%; Score 484; DB 21; Length 107;  
 Best Local Similarity 88.7%; Pred. No. 1.1e-26;

Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGRVITTCAROSISRYLWYQOKPEKAPRLIWSASNTQSGVPSRF 60  
 DB 1 ELTQSPSSLSASVGRVITTCAROSISRYLWYQOKPEKAPRLIWSASNTQSGVPSRF 60  
 QY 61 SSGSGCTEFTLTISNLOFEDFASVYCCQOSYTTLYTFGSGTKLEIKR 106  
 DB 61 SSGSGCTEFTLTISNLOFEDFATYCCQOSYTRPYTFGSGTKLEIKR 106  
 RESULT 6  
 AAG93590  
 ID AAG93590 standard; Protein; 107 AA.  
 XX  
 AC AAG93590;  
 XX  
 DT 14-SEP-2001 (first entry)  
 DE Human anti-Rh(D) chain I02 protein sequence.  
 XX  
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.  
 OS Homo sapiens.  
 XX  
 PN US6255455-B1.  
 PD 03-JUL-2001.  
 XX  
 PF 29-JAN-1999; 99US-0240274.  
 PR 11-OCT-1996; 96US-0028550.  
 PR 10-APR-1998; 98US-0081380.  
 PR 27-JUN-1997; 97US-0884045.  
 XX  
 PA (UYPR-) UNIV PENNSYLVANIA.  
 XX  
 PI Stegel DL;  
 DR WPI; 2001-388931/41.  
 DR N-PSDB; AAH68647.  
 XX  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine -  
 XX  
 PS Claim 1; Column 43; 162pp; English.  
 XX  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification  
 CC of the present invention.  
 CC  
 XX Sequence 107 AA;  
 SQ

Query Match 88.3%; Score 483; DB 22; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 1.3e-26;  
 Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGRVITTCAROSISRYLWYQOKPEKAPRLIWSASNTQSGVPSRF 60  
 DB 2 ELTQSPSSLSASVGRVITTCAROSISRYLWYQOKPEKAPRLIWSASNTQSGVPSRF 61  
 QY 61 SSGSGCTEFTLTISNLOFEDFASVYCCQOSYTTLYTFGSGTKLEIKR 106  
 DB 61 SSGSGCTEFTLTISNLOFEDFATYCCQOSYTRPYTFGSGTKLEIKR 106

Db 62 SSGSGGTDTFTLLTISLQPEDFATYCCQSYSTLMTFGGKTKEIKR 107

RESULT 7  
AAG3644  
ID AAG3644 standard; Protein; 107 AA.  
XX  
AC AAG3644;  
XX  
DT 14-SEP-2001 (first entry)  
XX  
DE Human anti-Rh(D) antibody clone SH13 protein sequence.  
XX  
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KM red blood cell; Rh phenotype; diagnosis; therapeutic.  
XX  
OS Homo sapiens.  
XX  
PN US6255455-B1.  
XX  
PD 03-JUL-2001.  
XX  
PF 29-JAN-1999; 99US-0240274.  
XX  
PR 11-OCT-1996; 96US-0028550.  
PR 10-APR-1998; 98US-0081380.  
PR 27-JUN-1997; 97US-0884045.  
XX  
PA (UNPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
DR WPI; 2001-388931/41.  
DR N-PSDB; AAH68701.  
XX  
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine -  
XX  
PS Claim 1; Column 68; 162pp; English.  
XX  
CC The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG3644 to AAG3669. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
CC AAG36558 to AAG3669, AAG3670 to AAG3697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 107 AA;  
XX

Query Match 87.8%; Score 480; DB 22; Length 107;  
Best Local Similarity 87.7%; Fred. No. 2.1e-26;  
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGRVTITTCAROSISTYLNWYQKPKAKLTIWASNLQSGVPSRF 60  
Db 2 ELTQSPSSLSASVGRVTITTCAROSISTYLNWYQKPKAKLTIWASNLQSGVPSRF 61  
Qy 61 SSGSGGTDTFTLLTISLQPEDFATYCCQSYSTLMTFGGKTKEIKR 106  
Db 62 SSGSGGTDTFTLLTISLQPEDFATYCCQSYSTLMTFGGKTKEIKR 107

RESULT 8  
AAR54261  
ID AAR54261 standard; protein; 107 AA.  
XX  
AC AAR54261;

XX 25-MAR-2003 (updated)  
DT 10-NOV-1994 (first entry)  
XX  
DE Anti-HIV gp120 immunoglobulin light chain variable region b27.  
XX  
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
KM neutralisation; monoclonal antibody; kappa light chain;  
KM variable region; framework; complementarity determining region.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FH Region  
FT 1..21  
FT /label= FR1  
FT 22..33  
FT /label= CDR1  
FT 34..48  
FT /label= FR2  
FT 49..55  
FT /label= CDR2  
FT 56..87  
FT /label= FR3  
FT 88..95  
FT /label= CDR3  
FT 96..107  
FT /label= FR4  
XX  
XX WO9407922-A1.  
XX  
XX 14-APR-1994.  
XX  
XX 30-SEP-1993; 93WO-US09328.  
XX  
XX 30-SEP-1992; 92US-0954148.  
XX  
XX (SCRI) SCRIPPS RES INST.  
XX  
PI Barbas CF, Burton DR, Lerner RA;  
XX  
XX WPI; 1994-135516/16.  
XX  
XX  
PT New human monoclonal antibodies neutralising HIV - react with  
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo  
PT or in vitro diagnosis and for passive immuno-therapy  
XX  
PS Claim 5; Page 190; 248pp; English.  
XX  
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR  
CC amplification using primers specific for heavy and light chain  
CC variable regions. The amplification products were inserted into a  
CC dicistronic vector to produce a library of fragments. E.coli XL1  
CC Blue cells were transformed with the library. Filamentous phage were  
CC produced which expressed the Mab regions on their surface. Panning  
CC with gp120 and gp41 resulted in the recovery of immunoreactive  
CC clones. The light chain VK region sequence AAR54261 neutralises HIV1  
CC gp120.  
CC (Updated on 25-MAR-2003 to correct FN field.)  
XX  
SQ Sequence 107 AA;  
XX

Query Match 87.0%; Score 476; DB 15; Length 107;  
Best Local Similarity 87.7%; Fred. No. 4.1e-26;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGRVTITTCAROSISTYLNWYQKPKAKLTIWASNLQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGRVTITTCAROSISTYLNWYQKPKAKLTIWASNLQSGVPSRF 60  
Qy 61 SSGSGGTDTFTLLTISLQPEDFATYCCQSYSTLMTFGGKTKEIKR 106  
Db 61 SSGSGGTDTFTLLTISLQPEDFATYCCQSYSTLMTFGGKTKEIKR 106

|    |   |   |
|----|---|---|
| XX | AAW01284  | standard; Protein; 107 AA.                          |
| XX | AAW01284  |   |
| XX | AAW01284  |   |
| XX | 29-JAN-1997   | (first entry)                                       |
| XX |   |   |
| XX | VL region of HIV neutralising Mab, clone b27.                         |   |
| XX |   |   |
| XX | Heavy chain; light chain; variable region; VH; monoclonal antibody;   |   |
| XX | MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;   |   |
| XX | virus infectivity assay; precursor gp160; immunocompetence; human;    |   |
| XX | anti-HIV antibody; detection; HIV infection.                          |   |
| XX |   |   |
| XX | Homo sapiens.   |   |
| XX |   |   |
| XX | Key   | Location/Qualifiers                                 |
| XX | Region  | 1..21   |
| XX | Region  | /label= FR1   |
| XX | Region  | 22..32  |
| XX | Region  | /label= CDR1  |
| XX | Region  | 33..47  |
| XX | Region  | /label= FR2   |
| XX | Region  | 48..54  |
| XX | Region  | /label= CDR2  |
| XX | Region  | 55..86  |
| XX | Region  | /label= FR3   |
| XX | Region  | 87..95  |
| XX | Region  | /label= CDR3  |
| XX | Region  | 96..107   |
| XX | Region  | /label= FR4   |
| XX |   |   |
| XX | WO9602273-A1.   |   |
| XX |   |   |
| XX | 01-FEB-1996.  |   |
| XX |   |   |
| XX | 11-JUL-1995;  | 95WO-US08743.                                       |
| XX |   |   |
| XX | 18-JUL-1994;  | 94US-0276852.                                       |
| XX |   |   |
| XX | (SCRI ) SCRIPPS RES INST.   |   |
| XX |   |   |
| XX | Barbas CF, Burton DR, Lerner RA;                                      |   |
| XX |   |   |
| XX | WPI, 1996-179601/18.  |   |
| XX |   |   |
| XX | Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in      |   |
| XX | passive immuno:therapy and detection of HIV infection.                |   |
| XX |   |   |
| XX | Example; Fig 11; 366pp; English.                                      |   |
| XX |   |   |
| XX | The sequences given in AAW01261-92 represent the light chain variable |   |
| XX | regions (VL) of a series of monoclonal antibodies (Mab's) which are   |   |
| XX | immunoreactive with HIV glycoprotein gp120 and are capable of         |   |
| XX | neutralising HIV. This sequence represents the sequence of the JK2    |   |
| XX | gene clone, b27. A Mab containing this VL sequence has the capacity   |   |
| XX | to reduce HIV infectivity titre in an in vivo virus infectivity assay |   |
| XX | by 50 % at a concentration of less than 700 ng of antibody/ml, and    |   |
| XX | binds mature gp120 preferentially over the precursor gp160. The Mab   |   |
| XX | may be used for determining immunocompetence of a human anti-HIV      |   |
| XX | antibody and in the detection of HIV infection.                       |   |
| XX |   |   |
| XX | Sequence  | 107 AA:   |
| XX |   |   |
| XX | Query Match   | 87.0%; Score 476; DB 17; Length 107;                |
| XX | Beat Local Similarity   | 87.7%; Pred. No. 4,1e-26;                           |
| XX | Matches   | 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0; |
| XX |   |   |
| XX | 1 ELTOSPSLSASVGRVITTCGARSISITXLMWYQOKGKAPKLLIMASASNOSGVPSRF           | 60  |
| XX | 1 ELTOSPSLSASVGRVITTCGARSISITXLMWYQOKGKAPKLLIYAASSISQSVPSRF           | 60  |

|                                      |   |    |   |     |
|--------------------------------------|---|----|---|-----|
| Oy                                   |   | 61 | SGSSGTEFTLTISNLOPEFPASYYCOQSYTLTTFSGGTLEIKR | 106 |
|                                      |   |    | :   |     |
| Dd                                   |   | 61 | SGSSGDTFTLTISSLPEDPFRATYCCQSISTPTFGGTLEIKR  | 106 |
|                                      |   |    | :   |     |
| RESULT 10                            |   |    |   |     |
| ID                                   | AA95136   |    |   |     |
| AC                                   | AA95136 standard; Protein: 107 AA.  |    |   |     |
| XX                                   | AA95136;  |    |   |     |
| CT                                   |   |    |   |     |
| DT                                   | 30-JUN-2000 (first entry)   |    |   |     |
| DE                                   | Anti-gp120 antibody light chain variable region from clone B27.           |    |   |     |
| KX                                   | Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;     |    |   |     |
| KM                                   | reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;      |    |   |     |
| KW                                   | glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.      |    |   |     |
| XX                                   | Homo sapiens.   |    |   |     |
| OS                                   |   |    |   |     |
| PN                                   | AU9948756-A.  |    |   |     |
| PD                                   | 17-FEB-2000.  |    |   |     |
| PF                                   | 16-SEP-1999; 99AU-0048756.  |    |   |     |
| PR                                   | 16-SEP-1999; 99AU-0048756.  |    |   |     |
| PS                                   | (SCRI ) SCRIPPS RES INST.   |    |   |     |
| PI                                   | Burton DR, Barbas CF, Lerner RA;  |    |   |     |
| DR                                   | WPI: 2000-293393/26.  |    |   |     |
| XX                                   |   |    |   |     |
| TX                                   | Novel human monoclonal antibodies which immunoreact with and neutralise   |    |   |     |
| TT                                   | human immunodeficiency virus useful for treating HIV infections -         |    |   |     |
| Example 9; Figure 11; 36pp; English. |   |    |   |     |
| XX                                   |   |    |   |     |
| XX                                   | The present sequence represents a fragment of an anti-human               |    |   |     |
| CC                                   | immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  |    |   |     |
| CC                                   | a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV    |    |   |     |
| CC                                   | mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  |    |   |     |
| CC                                   | gp160 and neutralises HIV and which reduces HIV infectivity titre in an   |    |   |     |
| CC                                   | in vitro virus infectivity assay by 50% at a concentration of less than   |    |   |     |
| CC                                   | 700 ng/ml. The antibodies are used as reagents for the diagnosis and      |    |   |     |
| CC                                   | immunotherapy of HIV induced disease. They are useful as neutralising     |    |   |     |
| CC                                   | field isolates and provide useful information regarding the               |    |   |     |
| CC                                   | immunocompetence of an immune response in HIV infected patients. The      |    |   |     |
| CC                                   | monoclonal antibodies are useful for producing anti-idiotypic antibodies  |    |   |     |
| CC                                   | which can be used to screen human monoclonal antibodies to identify       |    |   |     |
| CC                                   | whether the antibody has the same binding specificity as the antibodies   |    |   |     |
| CC                                   | of the invention. The neutralising antibodies define new epitopes on the  |    |   |     |
| CC                                   | HIV gp120 and gp41 glycoproteins, thus increasing the availability of new |    |   |     |
| CC                                   | immunotherapeutic human monoclonal antibodies. A major advantages of the  |    |   |     |
| CC                                   | monoclonal antibodies derives from the fact that they are encoded by a    |    |   |     |
| CC                                   | human polynucleotides sequence. Thus in vivo use of the monoclonal        |    |   |     |
| CC                                   | antibodies for diagnosis and immunotherapy of HIV induced disease greatly |    |   |     |
| CC                                   | reduces the problems of significant host immune response to the passively |    |   |     |
| CC                                   | administered antibodies which is a problem commonly encountered when      |    |   |     |
| CC                                   | monoclonal antibodies of xenogenic or chimeric derivation are utilized.   |    |   |     |
| CC                                   | An additional major advantage of the monoclonal antibodies described      |    |   |     |
| CC                                   | derives from the fact that they immunoreact with a unique determinant     |    |   |     |
| CC                                   | present on mature HIV glycoprotein gp120. This class of antibodies is     |    |   |     |
| CC                                   | particularly effective at neutralising field isolates of HIV.             |    |   |     |
| SQ                                   | Sequence 107 AA;  |    |   |     |
| Query March                          | 87.0%; Score 476; DB 21; Length 107;                                      |    |   |     |
| Best Local Similarity                | 87.7%; Pred. No. 4,1e-26;   |    |   |     |
| Matches 93; Conservative             | 8; Mismatches 5; Indels 0; Gaps 0,  |    |   |     |



QY 1 ELTQSPSSLSASVGDRTTTCARQISSTYINWYQKPKAKLLIMSASNLQSGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTTTCARQISSTYINWYQKPKAKLLIYAASSLQSGVPSRF 60  
 QY 61 SGSGGTFTLTISNLQFEDFASYYCOOSYTTLYTFGSGTLEIKR 106  
 DB 61 SGSGGTFTLTISNLQFEDFATYYCOOSYSTPTQFGGTLEIKR 106

RESULT 11  
 ID AAY98245  
 AA AAY98245 standard; Protein; 107 AA.  
 AC AAY98245;  
 XX  
 XX 04-JUL-2000 (first entry)  
 DT  
 DE Anti-gp120 antibody light chain variable region from clone B27.  
 XX  
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;  
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;  
 KW passive immunotherapy; reduce severity; HIV-induced disease;  
 KW immunocompetence; active immunisation.  
 XX  
 OS Homo sapiens.  
 XX  
 XX AU9948754-A.  
 XX  
 XX 17-FEB-2000.  
 PD  
 XX  
 XX 16-SEP-1999; 99AU-0048754.  
 PF  
 XX 16-SEP-1999; 99AU-0048754.  
 PR  
 XX (SCRI) SCRIPPS RES INST.  
 XX  
 XX PA  
 XX  
 PI Burton DR, Barbas CF, Lerner RA;  
 DR WPI; 2000-246867/22.  
 XX  
 XX Human neutralizing monoclonal antibodies to human immunodeficiency  
 PT virus (HIV) used for providing passive immunotherapy to HIV are  
 PT specific for glycoprotein-120 -  
 PT  
 XX Example 9; Figure 11; 374pp; English.  
 XX  
 XX This sequence represents a fragment of the antibodies of the invention.  
 CC The invention relates to the production of an anti-HIV (human  
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody  
 CC capable of reducing an HIV infectivity titre in an in vitro virus  
 CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The  
 CC method for the production of the antibody comprises:  
 CC (a) providing a first polynucleotide encoding a heavy chain  
 CC immunoglobulin amino acid sequence (which does not comprise the sequence  
 CC represented by AAY98206) and a second polynucleotide encoding a light  
 CC chain immunoglobulin amino acid sequence;  
 CC (b) inserting the first and second polynucleotide sequences into a host  
 CC cell;  
 CC (c) maintaining the host cell in conditions which allow the amino acid  
 CC sequences encoded by the polynucleotides to be expressed in the host  
 CC cell; and  
 CC (d) isolating the antibody comprising the heavy and light chain  
 CC immunoglobulin amino acid sequences from the host cell.  
 CC The anti-HIV gp-120 monoclonal antibody is used for providing passive  
 CC immunotherapy to HIV in a human. They can be administered to high-risk  
 CC patients to reduce the likelihood and/or severity of HIV-induced disease  
 CC and to patients who are already HIV-infected. The antibodies are used  
 CC for neutralising field isolates which provides information about the  
 CC immunocompetence of an immune response in HIV patients, for detecting  
 CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
 CC producing anti-idiotypic antibodies which can be used for active  
 CC immunisation and to screen human monoclonal antibodies to identify those

CC with the same binding specificity and to monitor the course of HIV  
 CC disease therapy by measuring the changes in concentration of HIV present  
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120  
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and  
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
 CC reduce the problems of significant host immune response to the  
 CC antibodies associated with monoclonal antibodies of xenogenic or  
 CC chimeric derivation.  
 XX  
 XX SQ Sequence 107 AA;  
 XX  
 XX Query Match 87.0%; Score 476; DB 21; Length 107;  
 XX Best Local Similarity 87.7%; Pred. No. 4.1e-26;  
 XX Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTTTCARQISSTYINWYQKPKAKLLIMSASNLQSGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTTTCARQISSTYINWYQKPKAKLLIYAASSLQSGVPSRF 60  
 QY 61 SGSGGTFTLTISNLQFEDFASYYCOOSYTTLYTFGSGTLEIKR 106  
 DB 61 SGSGGTFTLTISNLQFEDFATYYCOOSYSTPTQFGGTLEIKR 106

RESULT 12  
 ID AAG93663  
 AA AAG93663 standard; Protein; 107 AA.  
 AC AAG93663;  
 XX  
 XX 14-SEP-2001 (first entry)  
 DT  
 DE Human anti-Rh(D) antibody clone SH49 protein sequence.  
 XX  
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 XX US6255455-B1.  
 XX  
 XX 03-JUL-2001.  
 PD  
 XX  
 XX 29-JAN-1999; 99US-0240274.  
 PF  
 XX 11-OCT-1996; 96US-0028550.  
 PR 10-APR-1998; 98US-0081380.  
 PR 27-JUN-1997; 97US-0884045.  
 XX  
 XX (UNPE-) UNIV PENNSYLVANIA.  
 PA  
 PI Siegel DL;  
 DR WPI; 2001-388931/41.  
 DR N-PEDB; AAH68720.  
 XX  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine -  
 PT  
 XX Claim 1; Column 69; 162pp; English.  
 PS  
 XX The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (8) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification  
 CC of the present invention.

XX Sequence 107 AA;  
 SQ Query Match 86.8%; Score 475; DB 22; Length 107;  
 Best Local Similarity 85.8%; Pred. No. 4.8e-26;  
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDVITTCRARSISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60  
 DB 2 ELTGSPSSLSASVGDVITTCRARSISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 61  
 QY 61 SSGSGTTEFTLTITSLNQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
 DB 62 SSGSGTTEFTLTITSLNQFEDFATYYCOQSYSTPWTGQGTKEIKR 107

RESULT 13  
 AAG93664  
 ID AAG93664 standard; Protein; 107 AA.  
 AC AAG93664;  
 DT 14-SEP-2001 (first entry)  
 XX Human anti-Rh(D) antibody clone SH50 protein sequence.  
 DE Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX Homo sapiens.  
 OS US6255455-B1.  
 PN 03-JUL-2001.  
 PD 29-JAN-1999; 99US-0240274.  
 PF 11-OCT-1996; 96US-0028550.  
 PR 10-APR-1998; 98US-0081380.  
 PR 27-JUN-1997; 97US-0884045.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 PA Stegel DL;  
 PI WPI; 2001-388931/41.  
 DR N-PSDB; AAH68721.  
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine -  
 XX Claim 1; Column 69; 162pp; English.  
 PS The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (1) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification  
 CC of the present invention.  
 XX Sequence 107 AA;  
 SQ Query Match 86.8%; Score 475; DB 22; Length 107;  
 Best Local Similarity 85.8%; Pred. No. 4.8e-26;  
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDVITTCRARSISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60

DB 2 ELTGSPSSLSASVGDVITTCRARSISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 61  
 QY 61 SSGSGTTEFTLTITSLNQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
 DB 62 SSGSGTTEFTLTITSLNQFEDFATYYCOQSYSTPWTGQGTKEIKR 107

RESULT 14  
 AAG93667  
 ID AAG93667 standard; Protein; 107 AA.  
 AC AAG93667;  
 DT 14-SEP-2001 (first entry)  
 XX Human anti-Rh(D) antibody clone SH54 protein sequence.  
 DE Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX Homo sapiens.  
 OS US6255455-B1.  
 PN 03-JUL-2001.  
 PD 29-JAN-1999; 99US-0240274.  
 PF 11-OCT-1996; 96US-0028550.  
 PR 10-APR-1998; 98US-0081380.  
 PR 27-JUN-1997; 97US-0884045.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 PA Stegel DL;  
 PI WPI; 2001-388931/41.  
 DR N-PSDB; AAH68724.  
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine -  
 XX Claim 1; Column 70; 162pp; English.  
 PS The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (1) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification  
 CC of the present invention.  
 XX Sequence 107 AA;  
 SQ Query Match 86.7%; Score 474; DB 22; Length 107;  
 Best Local Similarity 85.8%; Pred. No. 5.6e-26;  
 Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDVITTCRARSISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60  
 DB 2 ELTGSPSSLSASVGDVITTCRARSISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 61  
 QY 61 SSGSGTTEFTLTITSLNQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
 DB 62 SSGSGTTEFTLTITSLNQFEDFATYYCOQSYSTPWTGQGTKEIKR 107

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RESULT 15
AAG93589
ID AAG93589 standard; Protein; 108 AA.
XX
AC AAG93589;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) chain I01 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-0240274.
XX
PR 11-OCT-1996; 96US-0028550.
PR 10-APR-1998; 98US-0081380.
PR 27-JUN-1997; 97US-0884045.
XX
PA (UNPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR MPI; 2001-388931/41.
DR N-PSDB; AAH68646.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine -
XX
PS Claim 1; Column 43; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification
CC of the present invention.
XX
SQ Sequence 108 AA;

Query Match 86.6%; Score 473.5; DB 22; Length 108;
Best Local Similarity 87.9%; Pred No. 6,1e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

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   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 ELTGSPSSISASVGRVITTCRARSISTYLNWYQOKPGKAPKLLIWSASNLQGVPSRF 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGGTETLTLSNLQFEDPASYYCQGSYTT-LTFPGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 SSGSGGTETLTLSNLQFEDPASYYCQGSYTPPYTFGGTKLEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Search completed: February 10, 2004, 18:36:11  
 Job time : 31.9606 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: February 10, 2004, 18:39:30 ; Search time 24.4121 Seconds  
(without alignments)  
909.160 Million cell updates/sec

Title: US-10-027-725A-11

Sequence: 1 ELTQSPSSLSASVGDRTVIT.....QQSTTLTYTFSGTKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                | Description       |
|------------|-------|-------------|--------|-------------------|-------------------|
| 1          | 547   | 100.0       | 106    | US-10-027-725A-11 | Sequence 11, Appl |
| 2          | 484   | 88.5        | 107    | US-10-016-986-104 | Sequence 104, App |
| 3          | 483   | 88.3        | 107    | US-09-848-798-33  | Sequence 33, Appl |
| 4          | 480   | 87.8        | 107    | US-09-848-798-156 | Sequence 156, App |
| 5          | 476   | 87.0        | 107    | US-10-016-986-105 | Sequence 105, App |
| 6          | 475   | 86.8        | 107    | US-09-848-798-175 | Sequence 175, App |
| 7          | 475   | 86.8        | 107    | US-09-848-798-179 | Sequence 179, App |
| 8          | 474   | 86.7        | 107    | US-09-848-798-176 | Sequence 176, App |
| 9          | 473.5 | 86.6        | 108    | US-09-848-798-32  | Sequence 32, Appl |
| 10         | 473.5 | 86.6        | 108    | US-09-848-798-43  | Sequence 43, Appl |
| 11         | 473   | 86.5        | 107    | US-09-848-798-37  | Sequence 37, Appl |
| 12         | 473   | 86.5        | 111    | US-10-203-754A-57 | Sequence 57, Appl |
| 13         | 472.5 | 86.4        | 108    | US-09-848-798-167 | Sequence 167, App |
| 14         | 472   | 86.3        | 107    | US-09-848-798-38  | Sequence 38, Appl |
| 15         | 472   | 86.3        | 107    | US-09-848-798-39  | Sequence 39, Appl |

|    |       |      |     |                   |                   |
|----|-------|------|-----|-------------------|-------------------|
| 16 | 472   | 86.3 | 107 | US-09-848-798-162 | Sequence 162, App |
| 17 | 471   | 86.1 | 107 | US-09-848-798-158 | Sequence 158, App |
| 18 | 469   | 85.7 | 107 | US-09-848-798-44  | Sequence 44, Appl |
| 19 | 468   | 85.6 | 111 | US-10-203-754A-56 | Sequence 56, Appl |
| 20 | 467   | 85.4 | 240 | US-09-192-854-2   | Sequence 2, Appl1 |
| 21 | 467   | 85.4 | 240 | US-09-968-561A-2  | Sequence 2, Appl1 |
| 22 | 467   | 85.4 | 240 | US-09-968-744A-2  | Sequence 2, Appl1 |
| 23 | 466   | 85.2 | 107 | US-09-791-153A-67 | Sequence 67, Appl |
| 24 | 465   | 85.0 | 107 | US-10-309-762-89  | Sequence 89, Appl |
| 25 | 464.5 | 84.9 | 108 | US-09-848-798-163 | Sequence 163, App |
| 26 | 463   | 84.6 | 104 | US-10-016-986-106 | Sequence 106, App |
| 27 | 463   | 84.6 | 107 | US-10-309-762-88  | Sequence 88, Appl |
| 28 | 462   | 84.5 | 127 | US-10-309-762-101 | Sequence 101, App |
| 29 | 460   | 84.1 | 106 | US-10-027-725A-10 | Sequence 10, Appl |
| 30 | 459   | 83.9 | 107 | US-09-848-798-168 | Sequence 168, App |
| 31 | 458   | 83.7 | 106 | US-10-377-121-5   | Sequence 5, Appl1 |
| 32 | 457   | 83.5 | 107 | US-09-848-798-36  | Sequence 36, Appl |
| 33 | 457   | 83.5 | 214 | US-10-153-382-19  | Sequence 19, Appl |
| 34 | 456.5 | 83.5 | 108 | US-09-848-798-41  | Sequence 41, Appl |
| 35 | 456.5 | 83.5 | 108 | US-10-016-986-109 | Sequence 109, App |
| 36 | 456   | 83.4 | 105 | US-10-309-762-155 | Sequence 155, App |
| 37 | 456   | 83.4 | 107 | US-09-848-798-173 | Sequence 173, App |
| 38 | 456   | 83.4 | 107 | US-10-309-762-67  | Sequence 67, Appl |
| 39 | 456   | 83.4 | 107 | US-10-309-762-68  | Sequence 68, Appl |
| 40 | 454   | 83.0 | 107 | US-10-016-986-103 | Sequence 103, App |
| 41 | 454   | 83.0 | 107 | US-10-364-743-54  | Sequence 54, App  |
| 42 | 453.5 | 82.9 | 114 | US-10-309-762-66  | Sequence 66, Appl |
| 43 | 453   | 82.8 | 107 | US-10-309-762-69  | Sequence 69, Appl |
| 44 | 453   | 82.8 | 107 | US-10-309-762-69  | Sequence 69, Appl |
| 45 | 453   | 82.8 | 108 | US-10-025-687-8   | Sequence 8, Appl1 |

## ALIGNMENTS

RESULT 1  
US-10-027-725A-11  
; Sequence 11, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Fliker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-11

Query Match 100.0%; Score 547; DB 15; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3.2e-42;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYNNWYQKPKKLIMASNLQGVPRF 60  
DB 1 ELTQSPSSLSASVGDRTVITCRAROSISTYNNWYQKPKKLIMASNLQGVPRF 60  
QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSQSYTTLYTFSGTKLEIKR 106  
DB 61 SGSGSGTEFTLTISNLQFEDFASYCQSQSYTTLYTFSGTKLEIKR 106

RESULT 2  
US-10-016-986-104  
; Sequence 104, Application US/10016986  
; Publication No. US20030187247A1  
; GENERAL INFORMATION:

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1  APPLICANT: Barton, Dennis R
2  APPLICANT: Barbas, Carlos F
3  APPLICANT: Jenner, Richard A
4  TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
5  TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
6  FILE REFERENCE: 313.2CON1
7  CURRENT APPLICATION NUMBER: US/10/016,986
8  CURRENT FILING DATE: 2001-12-12
9  PRIOR APPLICATION NUMBER: US 09/149,898
10 PRIOR FILING DATE: 1998-09-08
11 PRIOR APPLICATION NUMBER: US 08/899,575
12 PRIOR FILING DATE: 1997-07-24
13 PRIOR APPLICATION NUMBER: US 08/276,852
14 PRIOR FILING DATE: 1994-07-18
15 PRIOR APPLICATION NUMBER: US 08/178,302
16 PRIOR FILING DATE: 1994-01-06
17 PRIOR APPLICATION NUMBER: PCT/US93/09328
18 PRIOR FILING DATE: 1993-09-30
19 PRIOR APPLICATION NUMBER: US 07/954,148
20 PRIOR FILING DATE: 1992-09-30
21 NUMBER OF SEQ ID NOS: 176
22 SOFTWARE: FastSeq for Windows Version 4.0
23 SEQ ID NO 104
24 LENGTH: 107
25 TYPE: PRN
26 ORGANISM: Artificial Sequence
27 FEATURE:
28 OTHER INFORMATION: Synthesized
29 US-10-016-986-104

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| Best Local Similarity | 88.7%          | Pred No. 1.6e-36 |          |            |
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RESULT 3  
US-09-848-798-33

Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 FILE REFERENCE: 09596-42U2  
 CURRENT APPLICATION NUMBER: US/09/848,798

PRIOR APPLICATION NUMBER: 09/240,274  
 PRIOR FILING DATE: 1999-01-29  
 PRIOR APPLICATION NUMBER: 60/028,550

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; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
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; ZNAMEN: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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| Query Match      | 88.3% | Score 483 | DB 11 | Length 107 |
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| US-09-848-798-33 |       |           |       |            |
| US-09-848-798-33 |       |           |       |            |

|         |     |   |     |            |    |        |    |      |  |
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| Matches | 93; | Conservative  | 10; | Mismatches | 3; | Indels | 0; | Gaps |  |
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QY 61 SSGSGSGTEFTLLTISNLFEDFASYYQQQSYTLLYTSGSGTKLRIK 106

Db 62 SSGSGSGTDFLLTISLQPFEDFATYYQQQSYSTLMTGFGQGTKEIKR 107

RESULT 4  
US-09-848-798-156

Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: PL/CL BINDING PROTEINS AND MONOCLONALLY ACTIVATED CELLS

; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 ; FILE REFERENCE: 09596-42U2  
 ; CURRENT APPLICATION NUMBER: US/09/848,798  
 ; CURRENT PENDING NUMBER: 0903 OF 04

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1005 10 11

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; NUMBER OF SEQ ID NOS: 224
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156

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TYPE: PRT
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ORGANISM: Homo sapiens
FEATURE:

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| Matches | 93; Conservative | 9; Mismatches           | 4; Indels                       | 0; Gaps |
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Db 2 ELTGPSLSASVGDVITTCASQSISSYLNWYQQKPKGAPKLLIYAASSLRSGVSRF 6  
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Db 62 SSGSGTDFLTISSLPEDFAIYYCCQSYSTPYTGGCKLEIKR 107

US-10-016-986-105  
; Sequence 105, Application US/10016986  
; Publication No. US20030187247A1

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; APPLICANT: Burton, Dennis R
;
; APPLICANT: Barbas, Carlos F
;
; APPLICANT: Lerner, Richard A
;

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; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986

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PRIOR APPLICATION NUMBER: US 09/149,898  
PRIOR FILING DATE: 1998-09-08  
PRIOR APPLICATION NUMBER: US 08/899,575

PRIORITY FILING DATE: 1994-07-25  
 PRIORITY APPLICATION NUMBER: US 08/276,852  
 PRIORITY FILING DATE: 1994-07-18  
 PRIORITY APPLICATION NUMBER: US 08/178,302

PRIOR FILING DATE: 1994-01-06  
 PRIOR APPLICATION NUMBER: PCT/US93/09328  
 PRIOR FILING DATE: 1993-09-30  
 PRIOR APPLICATION NUMBER: US 07/954,148

; PRIOR FILING DATE: 1992-09-30  
 ;  
 ; NUMBER OF SEQ ID NOS: 176  
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 ; SOFTWARE: FastSeq for Windows, Version 4.0

SEQ ID NO 105  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized  
US-10-016-986-105

Query Match 87.0%; Score 476; DB 12; Length 107;  
Best Local Similarity 87.7%; Pred. No. 8.3e-36;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRYITTCRARSISTYINMWYQKRGKAPKLLIWSASNLQSGVPSRF 60  
DB 1 ELTQSPSSLSASVGDVRYITTCRARSISTYINMWYQKRGKAPKLLIYASLSQSGVPSRF 60  
QY 61 SGGSGTEFTLTISNLQEPEDFASYYCOOSYTTLYTFPGSGTKLEIKR 106  
DB 61 SGGSGGTDFTLTISLQEPEDFATYYCOOSYSTPTPFGGTKEIKR 106

RESULT 6  
US-09-848-798-175

Sequence 175, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 175  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-09-848-798-175

Query Match 86.8%; Score 475; DB 11; Length 107;  
Best Local Similarity 85.8%; Pred. No. 1e-35;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRYITTCRARSISTYINMWYQKRGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVRYITTCRARSISTYINMWYQKRGKAPKLLIYASLSQSGVPSRF 61  
QY 61 SGGSGTEFTLTISNLQEPEDFASYYCOOSYTTLYTFPGSGTKLEIKR 106  
DB 62 SGGSGGTDFTLTISLQEPEDFATYYCOOSYSTPTPFGGTKEIKR 107

RESULT 7  
US-09-848-798-176

Sequence 176, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 176  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
US-09-848-798-176

Query Match 86.8%; Score 475; DB 11; Length 107;  
Best Local Similarity 85.8%; Pred. No. 1e-35;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRYITTCRARSISTYINMWYQKRGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVRYITTCRARSISTYINMWYQKRGKAPKLLIYASLSQSGVPSRF 61  
QY 61 SGGSGTEFTLTISNLQEPEDFASYYCOOSYTTLYTFPGSGTKLEIKR 106  
DB 62 SGGSGGTDFTLTISLQEPEDFATYYCOOSYSTPTPFGGTKEIKR 107

RESULT 8  
US-09-848-798-179

Sequence 179, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 179  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-848-798-179

Query Match 86.7%; Score 474; DB 11; Length 107;  
Best Local Similarity 85.8%; Pred. No. 1.3e-35;  
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRYITTCRARSISTYINMWYQKRGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVRYITTCRARSISTYINMWYQKRGKAPKLLIYASLSQSGVPSRF 61  
QY 61 SGGSGTEFTLTISNLQEPEDFASYYCOOSYTTLYTFPGSGTKLEIKR 106  
DB 62 SGGSGGTDFTLTISLQEPEDFATYYCOOSYSTPTPFGGTKEIKR 107

RESULT 9  
US-09-848-798-32

Sequence 32, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04

RESULT13  
US-09-848-798-167  
; Sequence 167, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:



APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 167  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH34  
US-09-848-798-167

Query Match 86.4%; Score 472.5; DB 11; Length 108;  
Best Local Similarity 87.9%; Pred. No. 1.7e-35;  
Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 61  
QY 61 SSGSGTEFTLTISNLOPEDFASYYCOQSYTT-LYTFGSGTLEIKR 106  
DB 62 SSGSGTDTLTITISLQPEDFATYYCOQSYSTPRTFGGTVEIKR 108

RESULT 14  
US-09-848-798-38  
Sequence 38, Application US/09848798  
Publication No. US20030040605A1

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/848,798

PRIOR FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 09/240,274

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 60/028,550

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 38

LENGTH: 107

TYPE: PRT

ORGANISM: Homo sapiens

OTHER INFORMATION: anti-Rh(D) chain 107

US-09-848-798-38

Query Match 86.3%; Score 472; DB 11; Length 107;  
Best Local Similarity 86.8%; Pred. No. 1.9e-35;  
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 61

QY 61 SSGSGTEFTLTISNLOPEDFASYYCOQSYTTLYTFGSGTLEIKR 106  
DB 62 SSGSGTDTLTITISLQPEDFATYYCOQSYSTPRTFGGTVEIKR 107

RESULT 15  
US-09-848-798-39

Sequence 39, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 60/028,550  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 39  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 108  
US-09-848-798-39

Query Match 86.3%; Score 472; DB 11; Length 107;  
Best Local Similarity 86.8%; Pred. No. 1.9e-35;  
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVITTCRAQSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 61

QY 61 SSGSGTEFTLTISNLOPEDFASYYCOQSYTTLYTFGSGTLEIKR 106  
DB 62 SSGSGTDTLTITISLQPEDFATYYCOQSYSTPRTFGGTVEIKR 107

Search completed: February 10, 2004, 19:03:04  
Job time : 25.4121 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 ; Search time 10.9212 Seconds  
(without alignments)  
410.664 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547  
Sequence: 1 ELVQSPSSLSASVGDRTVIT.....QOSTYTLVTFSGTKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                          |
|------------|-------|-------------|--------|----|--------------------------------------|
| 1          | 484   | 88.5        | 107    | 1  | US-08-276-852-104 Sequence 104, App  |
| 2          | 484   | 88.5        | 107    | 1  | US-08-899-575-104 Sequence 104, App  |
| 3          | 484   | 88.5        | 107    | 1  | US-08-899-575-104 Sequence 104, App  |
| 4          | 484   | 88.5        | 107    | 5  | PCT-US95-08743-104 Sequence 104, App |
| 5          | 483   | 88.3        | 107    | 3  | US-09-240-274-33 Sequence 33, App1   |
| 6          | 480   | 87.8        | 107    | 3  | US-09-240-274-156 Sequence 156, App  |
| 7          | 476   | 87.0        | 107    | 1  | US-08-276-852-105 Sequence 105, App  |
| 8          | 476   | 87.0        | 107    | 1  | US-08-899-575-105 Sequence 105, App  |
| 9          | 476   | 87.0        | 107    | 1  | US-08-899-575-105 Sequence 105, App  |
| 10         | 476   | 87.0        | 107    | 5  | PCT-US95-08743-105 Sequence 105, App |
| 11         | 475   | 86.8        | 107    | 3  | US-09-240-274-175 Sequence 175, App  |
| 12         | 475   | 86.8        | 107    | 3  | US-09-240-274-176 Sequence 176, App  |
| 13         | 474   | 86.7        | 107    | 3  | US-09-240-274-179 Sequence 179, App  |
| 14         | 473.5 | 86.6        | 108    | 3  | US-09-240-274-32 Sequence 32, App1   |
| 15         | 473.5 | 86.6        | 108    | 3  | US-09-240-274-43 Sequence 43, App1   |
| 16         | 473   | 86.5        | 107    | 3  | US-09-240-274-37 Sequence 37, App1   |
| 17         | 472.5 | 86.4        | 108    | 3  | US-09-240-274-167 Sequence 167, App  |
| 18         | 472   | 86.3        | 107    | 3  | US-09-240-274-38 Sequence 38, App1   |
| 19         | 472   | 86.3        | 107    | 3  | US-09-240-274-39 Sequence 39, App1   |
| 20         | 472   | 86.3        | 107    | 3  | US-09-240-274-162 Sequence 162, App  |
| 21         | 471   | 86.1        | 107    | 3  | US-09-240-274-158 Sequence 158, App  |
| 22         | 469   | 85.7        | 107    | 3  | US-09-240-274-44 Sequence 44, App1   |
| 23         | 468   | 85.6        | 108    | 3  | US-08-379-057-29 Sequence 29, App1   |
| 24         | 464.5 | 84.9        | 108    | 3  | US-09-240-274-163 Sequence 163, App  |
| 25         | 463   | 84.6        | 104    | 1  | US-08-276-852-106 Sequence 106, App  |
| 26         | 463   | 84.6        | 104    | 1  | US-08-899-575-106 Sequence 106, App  |
| 27         | 463   | 84.6        | 104    | 1  | US-08-899-575-106 Sequence 106, App  |

|    |       |      |     |   |                    |                    |
|----|-------|------|-----|---|--------------------|--------------------|
| 28 | 463   | 84.6 | 104 | 5 | PCT-US95-08743-106 | Sequence 106, App  |
| 29 | 461   | 84.3 | 108 | 4 | US-09-025-769B-14  | Sequence 14, App1  |
| 30 | 459   | 83.9 | 107 | 1 | US-08-300-386A-66  | Sequence 66, App1  |
| 31 | 459   | 83.9 | 107 | 3 | US-08-931-645-66   | Sequence 66, App1  |
| 32 | 459   | 83.9 | 107 | 5 | US-09-240-274-168  | Sequence 168, App1 |
| 33 | 459   | 83.9 | 107 | 3 | PCT-US95-11235-66  | Sequence 66, App1  |
| 34 | 457   | 83.5 | 107 | 3 | US-09-240-274-36   | Sequence 36, App1  |
| 35 | 457   | 83.5 | 109 | 3 | US-09-157-370-3    | Sequence 3, App1   |
| 36 | 456.5 | 83.5 | 108 | 1 | US-08-276-852-109  | Sequence 109, App  |
| 37 | 456.5 | 83.5 | 108 | 1 | US-08-899-575-109  | Sequence 109, App  |
| 38 | 456.5 | 83.5 | 108 | 1 | US-08-899-575-109  | Sequence 109, App  |
| 39 | 456.5 | 83.5 | 108 | 3 | US-09-240-274-109  | Sequence 41, App1  |
| 40 | 456.5 | 83.5 | 108 | 3 | PCT-US95-08743-109 | Sequence 109, App  |
| 41 | 456   | 83.4 | 107 | 3 | US-09-240-274-173  | Sequence 173, App  |
| 42 | 454   | 83.0 | 107 | 1 | US-08-276-852-103  | Sequence 103, App  |
| 43 | 454   | 83.0 | 107 | 1 | US-08-899-575-103  | Sequence 103, App  |
| 44 | 454   | 83.0 | 107 | 1 | US-08-899-575-103  | Sequence 103, App  |
| 45 | 454   | 83.0 | 107 | 3 | US-09-240-274-40   | Sequence 40, App1  |

## ALIGNMENTS

RESULT 1  
US-08-276-852-104  
Sequence 104, Application US/08276852  
Patent No. 5652138  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESS: Patent Counsel  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
STREET: Mail Drop 7PC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-104

|                       |              |                    |               |             |
|-----------------------|--------------|--------------------|---------------|-------------|
| Query Match           | 88.5%        | Score 484;         | DB 1;         | Length 107; |
| Best Local Similarity | 88.7%        | Pred. No. 1.1e-36; |               |             |
| Matches 94;           | Conservative | 8;                 | Mismatches 4; | Indels 0;   |
|                       |              |                    | Gaps          | 0;          |

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Oy      1 ELTGSPSSLSASVGDRTITCRARQISITLYLNTYQQKPGAPAKLLIWSASNQSGVPSRF 600
        |||||
Db      1 ELTGSPSSLSASVGDRVTITCRASQSISSYLNTYQQKPKGAPAKLLIYAASSIQSGVPSRF 600
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QY      61 SGGSGTEFTLTISNLQFEDPASYYCCQSYTTLTFTGSGTKLEIKR 106
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Db      61 SGGSGTDTFTLTISLQEPFATYYCCQSYSTPYTFGGTKLEIKR 106

```

RESULT 2  
US-08-899-575-104

Patent No. 5770440

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS: The Scripps Research Institute, Office of  
 ADDRESSEE: Patent Counsel  
 ADDRESSEE: Patent Counsel  
 STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220  
 STREET: Mail Drop TPC8  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentln Release #1.0, Version #1.25

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1      CURRENT APPLICATION DATA:
2      APPLICATION NUMBER: US/08/899,575
3      FILING DATE: 24-JUL-1997
4      CLASSIFICATION: 435
5      PRIOR APPLICATION DATA:
6      APPLICATION NUMBER: US 08/276,852
7      FILING DATE: 18-JUL-1994
8      APPLICATION NUMBER: US 08/178,302
9      FILING DATE: 30-SEP-1993
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: US 07/954,148
12     FILING DATE: 30-SEP-1992
13     ATTORNEY/AGENT INFORMATION:
14     NAME: Fitting, Thomas
15     REGISTRATION NUMBER: 34,163
16     REFERENCE/DOCKET NUMBER: SCR1452P
17     TELECOMMUNICATION INFORMATION:
18     TELEPHONE: 619-554-2937
19     TELEFAX: 619-554-6312
20     INFORMATION FOR SEQ ID NO: 104:
21     SEQUENCE CHARACTERISTICS:
22     LENGTH: 107 amino acids
23     TYPE: amino acid
24     TOPOLOGY: linear
25     MOLECULE TYPE: protein
26     US-08-899-575-104

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|                       |       |  |      |            |
|-----------------------|-------|--|------|------------|
| Query Match           | 88.5% | Score 484  | DB 1 | Length 107 |
| Best Local Similarity | 88.7% | Pred. No. 1,1e-36  |      |            |
| Matches               | 94    | Conservative   | 4    | Indels 0   |
|                       |       |  |      | Gaps       |
| Qy                    | 1     | ELTSPSSLSASVGDRTYITTCRARQOSISTYTNWYQOKRGAAPKLLIWSASNLQGVPSRF |      | 6          |
| Db                    | 1     | ELTSPSSLSASVGDRTYITTCRARQOSISTYTNWYQOKRGAAPKLLIYAAASLQGVPSRF |      | 6          |

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OY      61  SSSSGTEFTLTISNLPEDFASYYCCQSTLTLYTFGSGTKLEIKR  106
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61  SSGSGGTDFTLTITSSLPEDFATYYCCQSYSTPYTFGGTKLEIKR  106

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RESULT 3  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
Date: 08/08/2004

? PATENT NO. 5804410  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Burton, Dennis R  
 ? APPLICANT: Barbas, Carlos F  
 ? APPLICANT: Iener, Richard A  
 ? TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 ? TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 ? NUMBER OF SEQUENCES: 170  
 ? CORRESPONDENCE ADDRESS:

ADDRESS: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ParentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: /600/600 .TTF

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? APPLICATION NUMBER: US/08/899,575
? FILING DATE: 24-JUL-1997
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/276,852
? FILING DATE: 18-JUL-1994
? APPLICATION NUMBER: US 08/178,302
? FILING DATE: 30-SEP-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/954,148
? FILING DATE: 30-SEP-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Fitting, Thomas
? REGISTRATION NUMBER: 34,163
? REFERENCE/DOCKET NUMBER: SCRI452P
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 619-554-2937
? TELEFAX: 619-554-6312
? INFORMATION FOR SEQ ID NO: 104:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 107 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-899-575-104

Query Match      88.5%: Score 484; DB 1; Length 107;
Best Local Similarity 88.7%: Pred. No. 1,1e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

```

| Qy | 1  | ELTOSPSLSASVGDRTVITTCRASQSI  | STYLMNYYOOKPGKAPKLLI | WASNSNTQSGVPSRF | 60 |
|----|----|--|----------------------|-----------------|----|
| Db | 1  | ELTOSPSLSASVGDRTVITTCRASQSI <th>STYLMNYYOOKPGKAPKLLI</th> <th>WASNSNTQSGVPSRF</th> <td>60</td> | STYLMNYYOOKPGKAPKLLI | WASNSNTQSGVPSRF | 60 |
| Qy | 61 | SGSSGSGTEFTLLTISNLOFEDFASVYCOQSYTTL  | LYTFGSGTKLEIKR       | 106             |    |
| Db | 61 | SGSSGSGTDFLLTISNLOFEDFATVYCOQSYSTPTV   | TGGQSTKLEIKR         | 106             |    |

RESULT 4  
PCT-US95-08743-104  
; Sequence 104, Application PC/TUS9508743

```

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match      88.5%; Score 484; DB 5; Length 107;
Best Local Similarity 88.7%; Pred. No. 1.1e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCARQSIQSYLYLNMWYQKRGKAPKLIWSASNLQSGVPSRF 60
    |||
Db 1 ELTQSPSSLSASVGDRTVITTCARQSIQSYLYLNMWYQKRGKAPKLIWSASNLQSGVPSRF 60
    |||

Qy 61 SSGSGGTEFTLTISNLQFEDFASYYCOQSYTTLTYTFGSGTKLEIKR 106
    |||
Db 61 SSGSGGTEFTLTISNLQFEDFATYYCOQSYSTPTTFGSGTKLEIKR 106
    |||

RESULT 5
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
; US-09-240-274-33

Query Match      88.3%; Score 483; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-36;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCARQSIQSYLYLNMWYQKRGKAPKLIWSASNLQSGVPSRF 60
    |||
Db 2 ELTQSPSSLSASVGDRTVITTCARQSIQSYLYLNMWYQKRGKAPKLIWSASNLQSGVPSRF 61
    |||

Qy 61 SSGSGGTEFTLTISNLQFEDFASYYCOQSYTTLTYTFGSGTKLEIKR 106
    |||
Db 62 SSGSGGTEFTLTISNLQFEDFATYYCOQSYSTPTTFGSGTKLEIKR 107
    |||
```

```

RESULT 6
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
; US-09-240-274-156

Query Match      87.8%; Score 480; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.4e-36;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCARQSIQSYLYLNMWYQKRGKAPKLIWSASNLQSGVPSRF 60
    |||
Db 2 ELTQSPSSLSASVGDRTVITTCARQSIQSYLYLNMWYQKRGKAPKLIWSASNLQSGVPSRF 61
    |||

Qy 61 SSGSGGTEFTLTISNLQFEDFASYYCOQSYTTLTYTFGSGTKLEIKR 106
    |||
Db 62 SSGSGGTEFTLTISNLQFEDFATYYCOQSYSTPTTFGSGTKLEIKR 107
    |||

RESULT 7
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-105

Query Match 87.0%; Score 476; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 5.5e-36;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAPQISITLYLNWYQKPKAPKLIWSASNLQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITTCRAPQISITLYLNWYQKPKAPKLIWSASNLQGVPSRF 60

QY 61 SSGSGCTEFTLTISNLOFEDFASYCCQSYTTLTYFGSGTKLEIKR 106  
DB 61 SSGSGCTDFTLTISLQPEDFATYCCQSYSTPQTFGQTKLEIKR 106

## RESULT 8

US-08-899-575-105  
Sequence 105, Application US/08899575  
Patent No. 5770440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Query Match 87.0%; Score 476; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 5.5e-36;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAPQISITLYLNWYQKPKAPKLIWSASNLQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITTCRAPQISITLYLNWYQKPKAPKLIWSASNLQGVPSRF 60

QY 61 SSGSGCTEFTLTISNLOFEDFASYCCQSYTTLTYFGSGTKLEIKR 106  
DB 61 SSGSGCTDFTLTISLQPEDFATYCCQSYSTPQTFGQTKLEIKR 106

## RESULT 9

US-08-899-575-105  
Sequence 105, Application US/08899575  
Patent No. 5804440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

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Query Match      87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.5e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISITLYLMWYQOKPKAKPLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRASQISITLYLMWYQOKPKAKPLIWSASNLQSGVPSRF 60

QY 61 SSGSGTEFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106
DB 61 SSGSGTEFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106

RESULT 10
PCT-US95-08743-105
; Sequence 105, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-105

Query Match      87.0%; Score 476; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.5e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISITLYLMWYQOKPKAKPLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRASQISITLYLMWYQOKPKAKPLIWSASNLQSGVPSRF 60

QY 61 SSGSGTEFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106
DB 61 SSGSGTEFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106

RESULT 11
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1999-01-29
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
```

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TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 6.8e-36;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISITLYLMWYQOKPKAKPLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITTCRASQISITLYLMWYQOKPKAKPLIWSASNLQSGVPSRF 61

QY 61 SSGSGTEFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106
DB 62 SSGSGTEFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 107

RESULT 12
US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Query Match      86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 6.8e-36;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISITLYLMWYQOKPKAKPLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITTCRASQISITLYLMWYQOKPKAKPLIWSASNLQSGVPSRF 61

QY 61 SSGSGTEFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106
DB 62 SSGSGTEFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 107

RESULT 13
US-09-240-274-179
; Sequence 179, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1999-01-29
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
```

```
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match      86.7%; Score 474; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 8.3e-36;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITTCRAPROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTITTCRAPROSISTYLNWYQOKPGKAPKLLIWAASSLQSGVPSRF 61

QY 61 SSGSGGTEFTLTISNLQFEDFASYCCOQSYTTLTYFGSGTKLEIKR 106
DB 62 SSGSGGTDFTLTISLQPEDFATYCCOQSYSTPMTFGGTKLEIKR 107

RESULT 14
US-09-240-274-32
; Sequence 32; Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-32

Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 9.3e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTITTCRAPROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTITTCRAPROSISTYLNWYQOKPGKAPKLLIWAASSLQSGVPSRF 61

QY 61 SSGSGGTEFTLTISNLQFEDFASYCCOQSYTTLTYFGSGTKLEIKR 106
DB 62 SSGSGGTDFTLTISLQPEDFATYCCOQSYSTPMTFGGTKLEIKR 108

RESULT 15
US-09-240-274-43
; Sequence 43; Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
```

```
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-43

Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 9.3e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTITTCRAPROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTITTCRAPROSISTYLNWYQOKPGKAPKLLIWAASSLQSGVPSRF 61

QY 61 SSGSGGTEFTLTISNLQFEDFASYCCOQSYTTLTYFGSGTKLEIKR 106
DB 62 SSGSGGTDFTLTISLQPEDFATYCCOQSYSTPMTFGGTKLEIKR 108
```

Search completed: February 10, 2004, 18:42:09  
Job time : 11.9212 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 10.9212 Seconds  
(without alignments)  
933.402 Million cell updates/sec

Title: US-10-027-725a-12

Sequence: 1 ELTQSPSSVSASVGDRTVIT.....QQANSFPYFGQTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:\*

1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 462   | 84.2        | 117    | 2     | S46376      |
| 2          | 462   | 84.2        | 125    | 2     | S40316      |
| 3          | 459   | 83.6        | 125    | 2     | S40333      |
| 4          | 455   | 82.9        | 125    | 2     | S40349      |
| 5          | 454.5 | 82.8        | 130    | 2     | S40336      |
| 6          | 454   | 82.7        | 130    | 2     | S40368      |
| 7          | 451   | 82.1        | 128    | 2     | S46372      |
| 8          | 451   | 82.1        | 131    | 2     | S40352      |
| 9          | 450   | 82.0        | 105    | 2     | S36266      |
| 10         | 447   | 81.4        | 127    | 2     | S40367      |
| 11         | 446   | 81.2        | 108    | 2     | S19674      |
| 12         | 446   | 81.2        | 132    | 2     | S38646      |
| 13         | 445   | 81.1        | 117    | 2     | S46371      |
| 14         | 444   | 80.9        | 123    | 2     | S40331      |
| 15         | 444   | 80.9        | 132    | 2     | S40334      |
| 16         | 443   | 80.7        | 108    | 2     | B49047      |
| 17         | 441   | 80.3        | 108    | 2     | S47182      |
| 18         | 441   | 80.3        | 109    | 2     | S31998      |
| 19         | 441   | 80.3        | 124    | 2     | S40318      |
| 20         | 439.5 | 80.1        | 108    | 2     | S30521      |
| 21         | 439   | 80.0        | 129    | 2     | S40369      |
| 22         | 437   | 79.6        | 107    | 2     | S36264      |
| 23         | 435.5 | 79.3        | 108    | 2     | S34007      |
| 24         | 435   | 79.2        | 108    | 1     | K1HUBN      |
| 25         | 434.5 | 79.1        | 107    | 2     | S36275      |
| 26         | 434   | 79.1        | 108    | 1     | K1HUMS      |
| 27         | 434   | 79.1        | 108    | 1     | S44122      |
| 28         | 433   | 78.9        | 117    | 2     | S21527      |
| 29         | 432   | 78.7        | 108    | 2     | S36283      |

|    |       |      |     |   |        |                     |
|----|-------|------|-----|---|--------|---------------------|
| 30 | 431.5 | 78.6 | 107 | 2 | S47183 | Ig kappa chain - h  |
| 31 | 431   | 78.5 | 107 | 2 | S36262 | Ig lambda chain V   |
| 32 | 428   | 78.0 | 107 | 2 | S36269 | Ig lambda chain V   |
| 33 | 427   | 77.8 | 109 | 2 | S31981 | Ig kappa chain - h  |
| 34 | 426.5 | 77.7 | 107 | 1 | K1HUBR | Ig kappa chain V-I  |
| 35 | 426   | 77.6 | 108 | 2 | S36277 | Ig lambda chain V   |
| 36 | 426   | 77.6 | 109 | 2 | S31979 | Ig lambda chain - h |
| 37 | 426   | 77.6 | 110 | 2 | PN0535 | Ig kappa chain V r  |
| 38 | 426   | 77.6 | 122 | 2 | S40370 | Ig kappa chain - h  |
| 39 | 426   | 77.6 | 141 | 2 | A49134 | Ig kappa chain V-I  |
| 40 | 424   | 77.2 | 107 | 2 | I69017 | anti-HIV envelope   |
| 41 | 424   | 77.2 | 108 | 1 | K1HUMK | Ig kappa chain V-I  |
| 42 | 424   | 77.2 | 129 | 1 | K1HUMK | Ig kappa chain pre  |
| 43 | 423   | 77.0 | 108 | 1 | K1HUMU | Ig kappa chain V-I  |
| 44 | 423   | 77.0 | 108 | 1 | K1HUCS | Ig kappa chain V-I  |
| 45 | 423   | 77.0 | 126 | 2 | S40335 | Ig kappa chain V-J  |

## ALIGNMENTS

## RESULT 1

S46376  
Ig kappa chain V-J region (T33-14) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C:Accession: S46376; S38649

R:Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chI) gene re

A:Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46376

A:Molecule type: mRNA

A:Residues: 1-117 <BEN>

A:Cross-references: EMBL:Z27177; NID:G415969; PIDN:CAA81701.1; PID:G415970

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:25-99/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 84.2%; Score 462; DB 2; Length 117;

Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTRASQGISWLAWYOHQPKKLLIYASSLSQGVPERF 60

DB 12 QMTQSPSSVSASISDRVITTCRASQDSSWLAWYQKPKKLLIYASSLSQGVPLRF 71

QY 61 SSGSGTDFSLTITSSLOPEDSATYTCOQANSFPYFGQTKVEIKR 106

DB 72 SSGSGTDFSLTITSSLOPEDSATYTCOQANSFPYFGQTKVEIKR 117

RESULT 2

S40316

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40316

R:Klein, R.; Jaenichen, R.; Zachau, H. G.

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLB>

A:Cross-references: EMBL:X72426

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:31-105/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 84.2%; Score 462; DB 2; Length 125;

Matches 85.8%; Pred. No. 2.2e-32;



EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination

A:Reference number: S46369; MUID:94313975; PMID:8035491

A:Accession: S46372

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-128 <BEN>

A:Cross-references: EMBL:Z27173

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 128;  
Best Local Similarity 83.8%; Pred. No. 1.9e-31;  
Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSASVGVGRVITTCRASOGISSWLMAMVQHOPKAKPLIYASLSIQGVPSRFS 61  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 24 LTQSPSSLSASGTGRVITTCRASOGISSYLMAYQOKPKAKPLIYASTLIQSGVPSRFS 83  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 GSGVGTDFSLTISLSIQFEDSATYYCCQANSPPYFGQTKVEIKR 106  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 84 GSGSGTDFTLTISLSIQSEDFATYYCOQYYSYPRFGQTKVEIKR 128  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8

S40352

Ig kappa chain V-DJ-C region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40352

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi gene and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40352

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <KLE>

A:Cross-references: EMBL:X72462; NID:G441392; PIDN:CAAS1130.1; PID:G441393

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 131;  
Best Local Similarity 83.0%; Pred. No. 1.9e-31;  
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVITTCRASOGISSWLMAYOHQKAKPKLIYASLSIQGVPSRF 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 23 QMTQSPSSLSASVGNRVITTCRASOGISSYLMAYQOKPKKLIYASTLIQSGVPSRF 82  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGVGTDFSLTISLSIQFEDSATYYCCQANSPPYFGQTKVEIKR 106  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 83 GSGSGTDFSLTISLSIQFEDVATYYCCQKXNSVPRFGQTKVEIKR 128  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9

S36266

Ig lambda chain V region (clone alpha-TNF-E1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000

C:Accession: S36266

R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J

EMBO J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries.

A:Reference number: S36256; MUID:93178448; PMID:7679990

A:Accession: S36266

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-105 <GRI>

A:Cross-references: EMBL:Z18840; NID:G33423; PIDN:CAA79292.1; PID:G939916

C:Superfamily: immunoglobulin V region; immunoglobulin homology

```

C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      82.0%; Score 450; DB 2; Length 105;
Best Local Similarity 85.3%; Pred. No. 1.9e-31;
Matches 87; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Oy 2 LTQSPSSVASVGDRTVITTCRASQGISWLAWOHQPKAPKLLIYSASSLSQGVPSRFS 61
Db 4 LTQSPSSVASVGDRTVITTCRASQGISWLAWOHQPKAPKLLIYSASSLSQGVPSRFS 63

Oy 62 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKE 103
Db 64 GSGSGTDFLTITISLQPEDFATYCCQANSFPIFFGQTKLE 105

RESULT 10
S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40367
A:Status: preliminary; translation not shown
A:Cross-references: EMBL:X72477
A:Molecule type: mRNA
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match      81.4%; Score 447; DB 2; Length 127;
Best Local Similarity 82.1%; Pred. No. 4.1e-31;
Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Oy 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAWOHQPKAPKLLIYSASSLSQGVPSRF 60
Db 20 QMTQSPSSLASVGDRTVITTCRASQGISWLAWOHQPKAPKLLIYAAASSLSQGVPSRF 79

Oy 61 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
Db 80 GSGSGTDFLTITISLQPEDFATYCCQANSYNTPTGQGTKEIKR 125

RESULT 11
S19674
Ig kappa chain V region (clone alpha-TEU9) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19674
R: Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 561-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19674
A:Molecule type: mRNA
A:Residues: 1-108 <MAR>
A:Cross-references: EMBL:X61642; NID:G37860; PIDN:CAA43823.1; PID:G1335386
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      81.2%; Score 446; DB 2; Length 108;
Best Local Similarity 82.9%; Pred. No. 4.2e-31;
Matches 87; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Oy 2 LTQSPSSVASVGDRTVITTCRASQGISWLAWOHQPKAPKLLIYSASSLSQGVPSRFS 61
Db 4 LTQSPSSLASVGDRTVITTCRASQGISWLAWOHQPKAPKLLIYAAASSLSQGVPSRFS 63

```

QY 62 GSGYGTDFSLTISLQPEDSATYVCOQANSFPYFGGKTVEIKR 106  
 C/Accession: S40331  
 Db 64 GSGSGTDFTLTISLQPEDFATYVCOQANSFPYFGGKTVEIKR 108

## RESULT 12

S38646  
 Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C/Accession: S38646  
 R/Beniston, C.; Chastagner, P.; Zouali, M.  
 Submitted to the EMBL Data Library, November 1993  
 A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.  
 A/Reference number: S38643  
 A/Accession: S38646  
 A/Status: preliminary  
 A/Molecule type: mRNA

A/Residues: 1-113 <BEN>  
 A/Cross-references: EMBL:Z27173; NID:g415961; PIDN:CAA81697.1; PID:g415962  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:40-114/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 446; DB 2; Length 132;  
 Best Local Similarity 82.9%; Pred. No. 5.1e-31;  
 Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDRTVITTCRASQGISWLMWYOHOPGKAPKLLIYSASSLSQGVPSRF 61  
 Ig kappa chain V-J region (T24-3) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000  
 C/Accession: S46371; S38645  
 R/Beniston, C.; Chastagner, P.; Zouali, M.  
 EMBL J. 13, 2951-2962, 1994  
 A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination  
 A/Reference number: S46369; MUID:94313975; PMID:8039491  
 A/Accession: S46371  
 A/Molecule type: mRNA

## RESULT 13

S46371  
 Ig kappa chain V-J region (T24-3) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000  
 C/Accession: S46371; S38645  
 R/Beniston, C.; Chastagner, P.; Zouali, M.  
 EMBL J. 13, 2951-2962, 1994  
 A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination  
 A/Reference number: S46369; MUID:94313975; PMID:8039491  
 A/Accession: S46371  
 A/Molecule type: mRNA

A/Residues: 1-117 <BEN>  
 A/Cross-references: EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PID:g415960  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 445; DB 2; Length 117;  
 Best Local Similarity 78.7%; Pred. No. 5.6e-31;  
 Matches 85; Conservative 14; Mismatches 7; Indels 2; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMWYOHOPGKAPKLLIYSASSLSQGVPSRF 60  
 Db 10 QMTQSPSTLSASVGDRTVITTCRASRSISTLWYQOKPKAPKLLIYASTLSQGVPSRF 69  
 QY 61 GSGYGTDFSLTISLQPEDSATYVCOQANSF--PYFGGKTVEIKR 106  
 Db 70 GSGSGTDFTLTISLQPEDFATYVCOQANSFPYFGGKTVEIKR 117

RESULT 14  
 S40331  
 Ig kappa chain - human  
 C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C/Accession: S40331  
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A/Reference number: S40312; MUID:94080891; PMID:8258341  
 A/Accession: S40331  
 A/Status: preliminary; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-123 <KLE>  
 A/Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 444; DB 2; Length 123;  
 Best Local Similarity 83.8%; Pred. No. 7.1e-31;  
 Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMWYOHOPGKAPKLLIYSASSLSQGVPSRF 60  
 Db 19 QMTQSPSTLSASVGDRTVITTCRASQGISWLMWYQOKPKAPKLLIYASTLSQGVPSRF 78  
 QY 61 GSGYGTDFSLTISLQPEDSATYVCOQANSFPYFGGKTVEIKR 105  
 Db 79 GSGSGTDFTLTISLQPEDFATYVCOQANSFPYFGGKTVEIKR 123

## RESULT 15

S40334  
 Ig kappa chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C/Accession: S40334  
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A/Reference number: S40312; MUID:94080891; PMID:8258341  
 A/Accession: S40334  
 A/Status: preliminary; translation not shown  
 A/Molecule type: mRNA

A/Residues: 1-132 <KLE>  
 A/Cross-references: EMBL:X72444  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 444; DB 2; Length 132;  
 Best Local Similarity 80.2%; Pred. No. 7.6e-31;  
 Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMWYOHOPGKAPKLLIYSASSLSQGVPSRF 60  
 Db 24 QLTQSPSTLSASVGDRTVITTCRASQGISWLMWYQOKPKAPKLLIYASTLSQGVPSRF 83  
 QY 61 GSGYGTDFSLTISLQPEDSATYVCOQANSFPYFGGKTVEIKR 106  
 Db 84 GSGSGTDFTLTISLQPEDFATYVCOQANSFPYFGGKTVEIKR 129

Search completed: February 10, 2004, 18:41:11  
 Job time : 11.9212 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 ; Search time 5.94242 Seconds  
(without alignments)  
838.855 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSASVGDRTVIT.....QQANSFPTFGGKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description        |
|------------|-------|-------------|--------|------------|--------------------|
| 1          | 435   | 79.2        | 108    | KV1V_HUMAN | P04430 homo sapien |
| 2          | 434   | 79.1        | 108    | KV1S_HUMAN | P01611 homo sapien |
| 3          | 426.5 | 77.7        | 107    | KV1D_HUMAN | P01596 homo sapien |
| 4          | 424   | 77.2        | 108    | KV1W_HUMAN | P01610 homo sapien |
| 5          | 424   | 77.2        | 129    | KV1G_HUMAN | P01631 homo sapien |
| 6          | 423   | 77.0        | 108    | KV1H_HUMAN | P01599 homo sapien |
| 7          | 423   | 77.0        | 108    | KV1F_HUMAN | P01598 homo sapien |
| 8          | 419   | 76.3        | 108    | KV1L_HUMAN | P01604 homo sapien |
| 9          | 419   | 76.3        | 108    | KV1O_HUMAN | P01607 homo sapien |
| 10         | 416   | 75.8        | 108    | KV1B_HUMAN | P01594 homo sapien |
| 11         | 413   | 75.2        | 108    | KV1J_HUMAN | P01605 homo sapien |
| 12         | 410   | 74.7        | 108    | KV1E_HUMAN | P01597 homo sapien |
| 13         | 408   | 74.3        | 108    | KV1A_HUMAN | P01593 homo sapien |
| 14         | 406   | 74.0        | 108    | KV1P_HUMAN | P01608 homo sapien |
| 15         | 405   | 73.8        | 108    | KV1I_HUMAN | P01601 homo sapien |
| 16         | 402   | 73.2        | 117    | KV1I_HUMAN | P01601 homo sapien |
| 17         | 401   | 73.0        | 108    | KV1N_HUMAN | P01606 homo sapien |
| 18         | 401   | 73.0        | 108    | KV1Y_HUMAN | P80362 homo sapien |
| 19         | 394   | 71.8        | 117    | KV1J_HUMAN | P01597 homo sapien |
| 20         | 393   | 71.6        | 108    | KV1C_HUMAN | P01595 homo sapien |
| 21         | 391   | 71.2        | 108    | KV1K_HUMAN | P01603 homo sapien |
| 22         | 385   | 70.1        | 108    | KV1Q_HUMAN | P01609 homo sapien |
| 23         | 385   | 70.1        | 129    | KV1X_HUMAN | P04432 homo sapien |
| 24         | 383   | 69.8        | 108    | KV5S_MOUSE | P01652 mus musculu |
| 25         | 380   | 69.2        | 108    | KV5Q_MOUSE | P01653 mus musculu |
| 26         | 376   | 68.5        | 108    | KV5T_MOUSE | P01653 mus musculu |
| 27         | 373   | 67.9        | 108    | KV5K_MOUSE | P01644 mus musculu |
| 28         | 370.5 | 67.5        | 109    | KV1E_HUMAN | P01612 homo sapien |
| 29         | 370   | 67.4        | 128    | KV5E_MOUSE | P01637 mus musculu |
| 30         | 368   | 67.0        | 108    | KV5L_MOUSE | P01645 mus musculu |
| 31         | 368   | 67.0        | 108    | KV5O_MOUSE | P01648 mus musculu |
| 32         | 368   | 67.0        | 134    | KV4C_HUMAN | P06314 homo sapien |
| 33         | 367.5 | 66.9        | 129    | KV3M_HUMAN | P18136 homo sapien |

|    |       |      |     |   |            |                    |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 366.5 | 66.8 | 129 | 1 | KV3L_HUMAN | P18135 homo sapien |
| 35 | 366   | 66.7 | 108 | 1 | KV5P_MOUSE | P01649 mus musculu |
| 36 | 366   | 66.7 | 108 | 1 | KV5R_MOUSE | P01651 mus musculu |
| 37 | 366   | 66.7 | 114 | 1 | KV4A_HUMAN | P01625 homo sapien |
| 38 | 364.5 | 66.4 | 109 | 1 | KV3D_HUMAN | P01622 homo sapien |
| 39 | 363.5 | 66.2 | 109 | 1 | KV3B_HUMAN | P01620 homo sapien |
| 40 | 363   | 66.1 | 108 | 1 | KV5M_MOUSE | P01646 mus musculu |
| 41 | 362   | 65.9 | 111 | 1 | KV3F_MOUSE | P01624 mus musculu |
| 42 | 361.5 | 65.8 | 109 | 1 | KV3J_HUMAN | P01624 homo sapien |
| 43 | 361.5 | 65.8 | 129 | 1 | KV3H_HUMAN | P04207 homo sapien |
| 44 | 361   | 65.8 | 108 | 1 | KV5N_MOUSE | P01647 mus musculu |
| 45 | 359   | 65.4 | 111 | 1 | KV3M_MOUSE | P01665 mus musculu |

## ALIGNMENTS

| RESULT 1   |   | ALIGNMENTS |                |
|--|---|------------|----------------|
| ID   | Query Match   | Standard   | PRT            |
| KV1V_HUMAN   |   |            |                |
| AC P04430  |   |            | 108 AA.        |
| DT 13-AUG-1987 (Rel. 05, Created)                                    |   |            |                |
| DT 13-AUG-1987 (Rel. 05, Last sequence update)                       |   |            |                |
| DT 15-JUL-1999 (Rel. 38, Last annotation update)                     |   |            |                |
| DE Ig kappa chain V-I region BAN.                                    |   |            |                |
| OS Homo sapiens (Human).   |   |            |                |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |   |            |                |
| OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.         |   |            |                |
| OX NCBI_TaxID=9606;  |   |            |                |
| RN [1]   |   |            |                |
| RP SEQUENCE.   |   |            |                |
| RX MEDLINE=86174817; PubMed=3083240;                                 |   |            |                |
| RA Dwtlet F.E., O'Connor T.P., Benson M.D.;                          |   |            |                |
| RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";  |   |            |                |
| RL Mol. Immunol. 23:73-78(1986).                                     |   |            |                |
| DR PIR: A01878; KIHUBN.  |   |            |                |
| DR HSSP: P80362; 1WTU.   |   |            |                |
| DR GO: GO:0005576; C:extracellular; NAS.                             |   |            |                |
| DR GO: GO:0003823; F:antigen binding activity; NAS.                  |   |            |                |
| DR GO: GO:0006955; P:immune response; NAS.                           |   |            |                |
| DR InterPro: IPR007110; IG-like.                                     |   |            |                |
| DR InterPro: IPR003006; IG_MHC.                                      |   |            |                |
| DR InterPro: IPR003596; IG_V.  |   |            |                |
| DR Pfam: PF00047; Ig_1.  |   |            |                |
| DR SMART: SM00406; IgV_1.  |   |            |                |
| DR PROSITE: PS00835; IG_LIKE; 1.                                     |   |            |                |
| KW Immunoglobulin V region; Amyloid.                                 |   |            |                |
| FT DOMAIN 1 23   |   |            | FRAMEWORK-1.   |
| FT DOMAIN 24 34  |   |            | FRAMEWORK-1.   |
| FT DOMAIN 35 49  |   |            | FRAMEWORK-2.   |
| FT DOMAIN 50 56  |   |            | FRAMEWORK-2.   |
| FT DOMAIN 57 88  |   |            | FRAMEWORK-3.   |
| FT DOMAIN 89 97  |   |            | FRAMEWORK-3.   |
| FT DOMAIN 98 107   |   |            | FRAMEWORK-4.   |
| FT DISULFID 23 88  |   |            | BY SIMILARITY. |
| FT NON_TER 108 108   |   |            |                |
| SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;                |   |            |                |
| Query Match  |   |            |                |
| Best Local Similarity 78.3%; Pred. No. 2.5e-38;                      |   |            |                |
| Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;        |   |            |                |
| QY   | 1 ELTQSPSSVSASVGDRTVITCRASQGISSTLAMYQHOPGKAPKLLIYSASSLSQGVPERF 60 |            |                |
| DB   | 3 QLTQSPSSLSASVGRVITTCRASQSYVNYAWFQKPKSLIYDASTLQSGVPSNF 62        |            |                |
| QY   | 61 SSGSGTDFSLTISLQPEDSATYCCOANSFPTFGGKVEIKR 106                   |            |                |
| DB   | 63 TGGSGTDFSLTISLQPEDPATYCCQYNSYPTFGGKVEIKR 108                   |            |                |
| RESULT 2   |   |            |                |
| KV1S_HUMAN   |   |            |                |

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ID   KV15_HUMAN          STANDARD;             PRT;             108 AA.
AC   P01611;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region W65.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81092279; PubMed=6778806;
RA   Kratzin H., Yang C., Krusche J.U., Hillebrand N.;
RT   "Preparative separation of the tryptic hydrolysate of a protein by
RT   high-pressure liquid chromatography. The primary structure of a
RT   monoclonal L-chain of k-type, subgroup I (Bence-Jones protein
RT   W65).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).
CC   -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC   PIR; A01877; K1HUMS.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KM   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN 1 23 34 35 49 50 56 57 88 89 97 98 107 108 108
FT   DOMAIN 24 34 35 49 50 56 57 88 89 97 98 107 108 108
FT   DOMAIN 24 34 35 49 50 56 57 88 89 97 98 107 108 108
FT   DISULFID 23 88
FT   NON_TER 108 108
SQ   SEQUENCE 108 AA; 11608 MW; 782B1A4649A60E45 CRC64;

Query Match 79.1%; Score 434; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 3.2e-38;
Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVSGDRVTTCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSVASVSGDRVTTCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 62
QY 61 SGGSGYGFSLTISLQFEDSATYVCOQANSFYTGQGTKEIKR 106
DB 63 SGGSGYGFSLTISLQFEDSATYVCOQANSFYTGQGTKEIKR 106

RESULT 3
KV15_HUMAN          STANDARD;             PRT;             107 AA.
ID   KV15_HUMAN
AC   P01556;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75075135; PubMed=4216454;
RA   Milstein C.P., Deverson E.V.;

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RT   "Primary structure of kappa light chain from a human myeloma
RT   protein.";
RL   Eur. J. Biochem. 49:377-391 (1974).
CC   -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC   MARKER.
CC   -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01864; K1HUMR.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KM   Immunoglobulin V region; Glycoprotein.
FT   CARBOHYD 28 28
FT   NON_TER 107 107
SQ   SEQUENCE 107 AA; 11703 MW; E1BF0DE9844C3346 CRC64;

Query Match 77.7%; Score 426.5; DB 1; Length 107;
Best Local Similarity 76.4%; Pred. No. 1.9e-37;
Matches 81; Conservative 15; Mismatches 9; Indels 1; Gaps 1;

QY 1 ELTQSPSSVASVSGDRVTTCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSVASVSGDRVTTCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 62
QY 61 SGGSGYGFSLTISLQFEDSATYVCOQANSFYTGQGTKEIKR 106
DB 63 SGGSGYGFSLTISLQFEDSATYVCOQANSFYTGQGTKEIKR 106

RESULT 4
KV15_HUMAN          STANDARD;             PRT;             108 AA.
ID   KV15_HUMAN
AC   P01610;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region W6A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Gont F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein W6A) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
CC   -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC   AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC   WALDENSTROM'S MACROGLOBULINEMIA.
DR   PIR; A01876; K1HUMS.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KM   Immunoglobulin V region; Monoclonal antibody.
FT   DOMAIN 1 23 24 34 35 49
FT   DOMAIN 1 23 24 34 35 49
SQ   SEQUENCE 107 AA; 11703 MW; E1BF0DE9844C3346 CRC64;

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FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match
Best Local Similarity 77.2%; Score 424; DB 1; Length 108;
Matches 82; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTOSPSVSASVGDRTVITTCRASQGISWLMAYOHOPGKAPKLLIYASASSLOSQVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRASQGISIRNDLTWYQKRGKAPKLLIYASASSLOSQVPSRF 62
QY 61 SGGSGYTDFTSLTISLQFEDSATYTCQANSFPYTFGGQTVKVEIKR 106
DB 63 SGGSGGTETFTLTISLQPEDPATYTCLOQNSFPMTFGQTVKVEIKR 108

RESULT 5
KV1W HUMAN STANDARD; PRT; 129 AA.
ID P04431;
AC 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G.; Combrato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006 (1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129

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SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2P9 CRC64;

Query Match
Best Local Similarity 77.2%; Score 424; DB 1; Length 129;
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTOSPSVSASVGDRTVITTCRASQGISWLMAYOHOPGKAPKLLIYASASSLOSQVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITTCRASQGISINLWYQKRGKAPKLLIYASASSLOSQVPSRF 84
QY 61 SGGSGYTDFTSLTISLQFEDSATYTCQANSFPYTFGGQTVKVEIKR 105
DB 85 SGGSGGTETFTLTISLQPEDPATYTCLOQNSFPMTFGQTVKVEIKR 129

RESULT 6
KV1G HUMAN STANDARD; PRT; 108 AA.
ID P01599;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J.; Watanabe S.; Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.".
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; KIHUGL.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK-1.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 56 FRAMEWORK-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 89 97 FRAMEWORK-3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match
Best Local Similarity 77.0%; Score 423; DB 1; Length 108;
Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTOSPSVSASVGDRTVITTCRASQGISWLMAYOHOPGKAPKLLIYASASSLOSQVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRASQGISIRNDLTWYQKRGKAPKLLIYASASSLOSQVPSRF 62
QY 61 SGGSGYTDFTSLTISLQFEDSATYTCQANSFPYTFGGQTVKVEIKR 106
DB 63 SGGSGGTETFTLTISLQPEDPATYTCLOQNSFPMTFGQTVKVEIKR 108

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RESULT 7
KV1L_HUMAN          STANDARD;          PRT;          108 AA.
ID   KV1L_HUMAN
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Hae.
OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hae): subdivision within
RT   subgroups."
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01868; KIHUHU.
DR   HSSP; P01607; 1WTU.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG_1like.
DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR003596; IG_V.
DR   Pfam; PF00047; IG_V.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN 1 23 FRAMEWORK-1.
FT   DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN 35 49 FRAMEWORK-2.
FT   DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN 57 88 FRAMEWORK-3.
FT   DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN 98 107 FRAMEWORK-4.
FT   DISULFID 23 88 BY SIMILARITY.
FT   NON_TER 108 108
SQ   SEQUENCE 108 AA; 11671 MW; 08D3A6160BD0618 CRC64;
Query Match 77.0%; Score 423; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 4,4e-37;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTITTCRASQGISSWLAMYQHOPGKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTITTCRASQGISSWLAMYQHOPGKAPKLLIYSASSLSQGVPSRF 62
QY 61 SSGSGYTDPSLTITSSIQFEDSATYTCQANSPTFGQGTKEIKR 106
DB 63 SSGSGTIDPSLTITSSIQFEDSATYTCQANSPTFGQGTKEIKR 108

RESULT 8
KV1L_HUMAN          STANDARD;          PRT;          108 AA.
ID   KV1L_HUMAN
AC   P01558;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region EU.
OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.

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RX   MEDLINE=71064023; PubMed=5489770;
RA   Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT   acid sequence of the light chain."
RL   Biochemistry 9:3155-3161(1970).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds."
RL   Biochemistry 9:3188-3196(1970).
CC   -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A90562; KIHUHU.
DR   HSSP; P01607; 1REI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG_1like.
DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR003596; IG_V.
DR   Pfam; PF00047; IG_V.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN 1 23 FRAMEWORK-1.
FT   DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN 35 49 FRAMEWORK-2.
FT   DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN 57 88 FRAMEWORK-3.
FT   DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN 98 107 FRAMEWORK-4.
FT   DISULFID 23 88
FT   NON_TER 108 108
SQ   SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;
Query Match 76.3%; Score 419; DB 1; Length 108;
Best Local Similarity 76.2%; Pred. No. 1.1e-36;
Matches 80; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTITTCRASQGISSWLAMYQHOPGKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTITTCRASQGISSWLAMYQHOPGKAPKLLIYSASSLSQGVPSRF 62
QY 61 SSGSGYTDPSLTITSSIQFEDSATYTCQANSPTFGQGTKEIKR 105
DB 63 ISSGSGTEFTLTITSSIQFEDSATYTCQANSPTFGQGTKEIKR 107

RESULT 9
KV1L_HUMAN          STANDARD;          PRT;          108 AA.
ID   KV1L_HUMAN
AC   P01604;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Kue.
OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79237924; PubMed=112021;
RA   Bulitz M., Kley H.-P., Zeitler H.-J.;
RT   "The primary structure of the Bence-Jones protein Kue. The amino acid
RT   sequence of the variable part of a human L-chain of the kappa-type."
RL   Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC   -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01870; KIHUHU.
DR   HSSP; P01607; 1REI.

```



DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90EA898 CRC64;  
 Query Match 76.3%; Score 419; DB 1; Length 108;  
 Best Local Similarity 73.6%; Pred. No. 1.1e-36;  
 Matches 78; Conservative 16; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 ELTOSPSVSASVGDRTTCRASQGISSWLAWQHOGKAPKLLIYSASSLSQGVPSRF 60  
 DB 3 QMTOSPSSTOPASVGRVITTCRASQISINILWYQCKEAKKLLIYKASTLETGVPSRF 62  
 QY 61 SSGSGYGTDFSLTISLQFEDSATYVYCOQANSFPYTFGQTKVEIKR 106  
 DB 63 SSGSGGTERTLTINSLQPDPAFYTCQOYSRYPYTFGQTKDIR 108  
 RESULT 10  
 ID KV10 HUMAN STANDARD; PRT; 108 AA.  
 AC P01607;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-I region Rel.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=76023758; PubMed=809329;  
 RA Palm W.; Hilschmann N.;  
 RT "The primary structure of a crystalline monoclonal immunoglobulin  
 RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation  
 RT and characterization of the tryptic peptides; the complete amino acid  
 RT sequence of the protein; a contribution to the elucidation of the  
 RT three-dimensional structure of antibodies, in particular their  
 RT combining site.";  
 RT Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
 RL [2]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RP MEDLINE=76039968; PubMed=118211;  
 RA Bpp O.; Latman E.E.; Schiffer M.; Huber R.; Palm W.;  
 RT "The molecular structure of a dimer composed of the variable portions  
 RT of the Bence-Jones protein Rel refined at 2.0-A resolution.";  
 RT Biochemistry 14:4943-4952(1975).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A91663; KIHURE.  
 DR PDB; 1REI; 17-FEB-84.  
 DR PDB; 1AR2; 12-NOV-97.  
 DR PDB; 1BMW; 29-DEC-99.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT TURN 15 16  
 FT STRAND 19 25  
 FT TURN 30 31  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 44 49  
 FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 85 90  
 FT STRAND 97 98  
 FT STRAND 102 106  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;  
 Query Match 75.8%; Score 416; DB 1; Length 108;  
 Best Local Similarity 75.5%; Pred. No. 2.3e-36;  
 Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
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 DB 3 QMTOSPSLSASVGRVITTCRASQDILIKYINLQOIFGKAPKLLIYKASTLETGVPSRF 62  
 QY 61 SSGSGYGTDFSLTISLQFEDSATYVYCOQANSFPYTFGQTKVEIKR 106  
 DB 63 SSGSGGTERTLTINSLQPDPAFYTCQOYSRYPYTFGQTKDIR 108  
 RESULT 11  
 ID KV1B HUMAN STANDARD; PRT; 108 AA.  
 AC P01594;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-I region AU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=72189444; PubMed=5028201;  
 RA Schiechl H.; Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 RT protein AU)."  
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
 RL [2]  
 RN X-RAY CRYSTALLOGRAPHY.

RX MEDLINE=77022433; PubMed=1234024;  
RA Fehlgamer H., Schiffert M., Epp O., Colman P.M., Lattman E.E.,  
RA Schwager P., Seigelmann W., Schramm H.J.,  
RT "The structure determination of the variable portion of the  
RT Bence-Jones protein Au."  
RL Biophys. Struct. Mech. 1:139-146(1975).  
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
CC REGION OF THE KAPPA CHAIN REI.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A91653; KIHUAV.  
DR PDB; 1JVS; 30-JAN-02.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11939 MW; E801187BE6F6B9 CRC64;  
  
Query Match 75.2%; Score 413; DB 1; Length 108;  
Best Local Similarity 75.5%; Pred. No. 4.7e-36;  
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
  
QY 1 ELTQSSSVASVGVDRITTCRASQGISLWLYQHOPKAPKLLIYSASSLSQGVPSRF 60  
DB 3 QMTQSSSVASVGVDRITTCRASQGISLWLYQHOPKAPKLLIYSASSLSQGVPSRF 62  
QY 61 SSGSGYTDFTLTISSLOPEDSATYVCOQANSPPYFGQGTKEIKR 106  
DB 63 SSGSGYTDFTLTISSLOPEDSATYVCOQANSPPYFGQGTKEIKR 108  
  
RESULT 12  
KV1M\_HUMAN STANDARD; PRT; 108 AA.  
ID 21-JUL-1986 (Rel. 01, Created)  
AC P01605;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG kappa chain V-I region Lay.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
OX [1]  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77038198; PubMed=824717;  
RA Capra J.D., Klapper D.G.,  
RT "Complete amino acid sequence of the variable domains of two human  
RT Igm anti-gamma globulins (Lay/Pom) with shared idiotypic  
RT specificities."  
RL Scand. J. Immunol. 5:677-684(1976).  
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS  
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN PGM V-IT KAPPA CHAIN,  
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
CC GLOBULIN ACTIVITY.  
CC PIR; A01871; KIHULV.

DR HSSP; P01607; 1REI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11834 MW; 73993A95431434A CRC64;  
  
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Matches 77; Conservative 16; Mismatches 13; Indels 0; Gaps 0;  
  
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DB 3 QMTQSSSVASVGVDRITTCRASQGISLWLYQHOPKAPKLLIYSASSLSQGVPSRF 62  
QY 61 SSGSGYTDFTLTISSLOPEDSATYVCOQANSPPYFGQGTKEIKR 106  
DB 63 SSGSGYTDFTLTISSLOPEDSATYVCOQANSPPYFGQGTKEIKR 108  
  
RESULT 13  
KV1E\_HUMAN STANDARD; PRT; 108 AA.  
ID 21-JUL-1986 (Rel. 01, Created)  
AC P01587;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG kappa chain V-I region DEE.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
OX [1]  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72053133; PubMed=5124396;  
RA Milstien C.P., Deverson E.V.,  
RT "The amino acid sequence of a human kappa light chain."  
RL Biochem. J. 123:945-958(1971).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
DR HSSP; P01607; 1REI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 FRAMEWORK-4.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON TER 108 108

Search completed: February 10, 2004, 18:36:31  
Job time : 5.94242 secs

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|   |   |   |              |
|---|---|---|--------------|
| Dd  | 3   | QMTGSPSSLSASVGDVRVTITTCRASGSGISGNILAWYQKRGKVPKSLITYAASLTLSQGVPERF | 62           |
| Oy  | 61  | SGSGYGTDPSLTISSLQPEDSATYYCCQANSEPFYFGCGTKEIKR                     | 106          |
| Dd  | 63  | SGSGGCTDFTLTISLQPEDVATYYCCKYNAPRFEGTGLEIKR                        | 108          |
| <br>RESULT 2  |   |   |              |
| ID  | Q9UL77  | PRELIMINARY;  | PRT; 108 AA. |
| AC  | Q9UL77;   |   |              |
| DT  | 01-MAY-2000 (TREMBLrel. 13, Created)  |   |              |
| DT  | 01-MAY-2000 (TREMBLrel. 13, Last sequence update)   |   |              |
| DT  | 01-MAR-2003 (TREMBLrel. 23, Last annotation update)   |   |              |
| DE  | Mysin-reactive immunoglobulin light chain variable region<br>(Fragment).  |   |              |
| OS  | Homo sapiens (Human).   |   |              |
| OC  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |   |              |
| OX  | NCBI_TaxID=9606;  |   |              |
| RN  | [1]   |   |              |
| RP  | SEQUENCE FROM N.A.  |   |              |
| RX  | MEDLINE=98277139; PubMed=9614934;   |   |              |
| RA  | Yu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,<br>Young D.C.;  |   |              |
| RT  | "Mysin-reactive autoantibodies in rheumatic carditis and normal<br>fetuses";  |   |              |
| RL  | Clin. Immunol. Immunopathol. 87:184-192(1998).  |   |              |
| DR  | EMBL; AF035037; AAD56273.1; -.  |   |              |
| DR  | HSSP; P01607; IREI.   |   |              |
| DR  | InterPro; IPR007110; Ig-like.   |   |              |
| DR  | InterPro; IPR003006; IG_MHC.  |   |              |
| DR  | InterPro; IPR003596; IG_v.  |   |              |
| DR  | Pfam; PF00047; Ig_1.  |   |              |
| DR  | SMART; SM00406; IGV; 1.   |   |              |
| DR  | PROSITE; PS00835; IG_LIKE; 1.   |   |              |
| FT  | NON_TER   | 1   | -1           |
| FT  | NON_TER   | 108   | 108          |
| SQ  | SEQUENCE  | 108 AA; 11738 MW; C06681716C4D16F3 CRC64;                         |              |
| <br>Query Match                79.6%; Score 437; DB 4; Length 108;<br>Best Local Similarity     81.1%; Pred. No. 6, le-39;<br>Matches      86; Conservative    10; Mismatches    10; Indels    0; Gaps    0 |   |   |              |
| Oy  | 1   | ELTQSPSSVSASVGDVRVTITTCRASGGSISWLMWOHQPGAKPLIYSASSLSQGVSPRF       | 60           |
| Dd  | 3   | QMTGSPSSLSASVGDVRVTITTCRASGISISYLWYQKRGKAPNLIIYAASLSQGVSPRF       | 62           |
| Oy  | 61  | SGSGYGTDPSLTISSLQPEDSATYYCCQANSEPFYFGCGTKEIKR                     | 106          |
| Dd  | 63  | SGSGGCTDFTLTISLQPEDVATYYCOOYSTSWTFEGGTKEIKR                       | 108          |
| <br>RESULT 3  |   |   |              |
| ID  | Q9UL79  | PRELIMINARY;  | PRT; 108 AA. |
| AC  | Q9UL79;   |   |              |
| DT  | 01-MAY-2000 (TREMBLrel. 13, Created)  |   |              |
| DT  | 01-MAY-2000 (TREMBLrel. 13, Last sequence update)   |   |              |
| DT  | 01-MAR-2003 (TREMBLrel. 23, Last annotation update)   |   |              |
| DE  | Mysin-reactive immunoglobulin light chain variable region<br>(Fragment).  |   |              |
| OS  | Homo sapiens (Human).   |   |              |
| OC  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |   |              |
| OX  | NCBI_TaxID=9606;  |   |              |
| RN  | [1]   |   |              |
| RP  | SEQUENCE FROM N.A.  |   |              |
| RX  | MEDLINE=98277139; PubMed=9614934;   |   |              |
| RA  | Yu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,<br>Young D.C.;  |   |              |
| RT  | "Mysin-reactive autoantibodies in rheumatic carditis and normal<br>fetuses";  |   |              |

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BL Cln. Immunol. Immunopathol. 87:184-192(1998).
DR EML; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER
FT NON TER
SQ SEQUENCE 108 AA; 11787 MW; DB548F19724FBAE CRC64;

Query Match 79.1%; Score 434; DB 4; Length 108;
Best Local Similarity 81.0%; Pred. No. 1,3e-38;
Matches 85; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

OY 2 LTQSPSSVSASVGDVVTITCRASGGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 61
DB 4 MTQSPSLSLASVGRVITISCMMSGISSTLAWYQKRGKAPPELLIYASTLSQGVPSRF 63
OY 62 GSGYGTDPSSLTISLQFEDSATYTCQANSPFTYFGGTVEIKR 106
DB 64 GSGSGTDPFTLTISLQSEDFATYCCQYSPFPFGGTVEIKR 108

RESULT 4
O96SA9 PRELIMINARY; PRT; 107 AA.
ID AC O96SA9;
AC O96SA9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Anti-streptococcal/anti-mysin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96375893; PubMed=9712075;
RA Adderson E.E., Shikham A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mysin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER
FT NON TER
SQ SEQUENCE 107 AA; 11520 MW; 4AB43B9C5B577F16 CRC64;

Query Match 77.7%; Score 426.5; DB 4; Length 107;
Best Local Similarity 82.1%; Pred. No. 7,9e-38;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

OY 1 ELTQSPSSVSASVGDVVTITCRASGGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSLASVGRVITITCRASGGISSTLAWYQKRGKAPPELLIYASTLSQGVPSRF 62
OY 61 GSGYGTDPSSLTISLQFEDSATYTCQANSPFTYFGGTVEIKR 106
DB 63 GSGSGTDPFTLTISLQSEDFATYCCQYSPFPFGGTVEIKR 107

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ID Q9UL81 PRELIMINARY; PRT; 107 AA.  
AC Q9UL81;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Lin B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RL EMBL; AF035033; AAD56269.1; -.  
DR HSSP; P01607; 1REI.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 75.0%; Score 411.5; DB 4; Length 107;  
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Matches 82; Conservative 11; Mismatches 12; Indels 1; Gaps 1;  
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DB 3 QMTQSPSSVASVGRVITTCRASQGISWLMAYOHQPKKLIYSASLSQGVPSRF 62  
QY 61 GSGGVTDFSLTISLQFEDSATYTCQOANSFPYFGQTKVEIKR 106  
DB 63 GSGSGCTDFTLTISLQFEDPATYTCQOANSFPYFGQTKVEIKR 107

RESULT 6  
Q9RLA5 PRELIMINARY; PRT; 214 AA.  
AC Q9RLA5;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Kappa light chain of Mab7 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";  
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF152371; AAD40242.1; -.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON\_TER 1  
FT NON\_TER 1

FT NON\_TER 214  
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDB995E2A CRC64;  
Query Match 69.9%; Score 384; DB 11; Length 214;  
Best Local Similarity 67.0%; Pred. No. 6e-33;  
Matches 71; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGRVITTCRASQGISWLMAYOHQPKKLIYSASLSQGVPSRF 60  
DB 3 QMTQSPSSVASVGRVITTCRASQGISWLMAYOHQPKKLIYSASLSQGVPSRF 62  
QY 61 GSGGVTDFSLTISLQFEDSATYTCQOANSFPYFGQTKVEIKR 106  
DB 63 GSGSGCTDFTLTISLQFEDPATYTCQOANSFPYFGQTKVEIKR 108

RESULT 7  
Q9UL83 PRELIMINARY; PRT; 108 AA.  
AC Q9UL83;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Lin B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RL EMBL; AF035031; AAD56267.1; -.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 69.6%; Score 382; DB 4; Length 108;  
Best Local Similarity 65.7%; Pred. No. 4.3e-33;  
Matches 69; Conservative 21; Mismatches 15; Indels 0; Gaps 0;  
QY 2 LTQSPSSVASVGRVITTCRASQGISWLMAYOHQPKKLIYSASLSQGVPSRF 61  
DB 4 MTQSPATISVSPGRATISCRASQGISWLMAYOHQPKKLIYSASLSQGVPSRF 63  
QY 62 GSGGVTDFSLTISLQFEDSATYTCQOANSFPYFGQTKVEIKR 106  
DB 64 GSGSGCTDFTLTISLQFEDPATYTCQOANSFPYFGQTKVEIKR 108

RESULT 8  
Q8NEK1 PRELIMINARY; PRT; 234 AA.  
AC Q8NEK1;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.





FT NON TER 1 1  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match  
 Best Local Similarity 66.7%; Score 366; DB 11; Length 108;  
 Matches 68; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDVVTITTCRASQGISMTLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 61  
 DB 4 MTQSGTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 106  
 DB 64 GSGSGTDTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 108

## RESULT 12

Q91WS9 PRELIMINARY; PRT; 233 AA.

AC Q91WS9; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical 25.8 kDa protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC Tissue=Colon;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013496; AAH13496.1; -  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16B CRC64;

Query Match  
 Best Local Similarity 66.5%; Score 365; DB 11; Length 233;  
 Matches 71; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVVTITTCRASQGISMTLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60  
 DB 22 QMTQTSSLSASLIGRVITSCSGSQGIANYLWYQKPGVTKLLIYTSLSHSVPSRF 81  
 QY 61 GSGSGTDTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 106  
 DB 82 GSGSGTDTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 127

## RESULT 13

Q91WF8 PRELIMINARY; PRT; 234 AA.

AC Q91WF8; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical 25.9 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC Tissue=Colon;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC015292; AAH15292.1; -  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR InterPro; IPR001865; Ribosomal\_S2.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; 1.  
 KW Hypothetical protein.

QY 2 LTQSPSSVSASVGDVVTITTCRASQGISMTLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60  
 DB 4 MTQSGTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 106  
 DB 64 GSGSGTDTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 108

Query Match  
 Best Local Similarity 66.5%; Score 365; DB 11; Length 234;  
 Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVVTITTCRASQGISMTLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60  
 DB 23 QMTQTSSLSASLIGRVITSCRASQDISNYLWYQKPGVTKLLIYTSLSHSVPSRF 82  
 QY 61 GSGSGTDTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 106  
 DB 83 GSGSGTDTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 128

## RESULT 14

Q9UL78 PRELIMINARY; PRT; 109 AA.

AC Q9UL78; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Young D.C.;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
 RL EMBL; AF035036; AAD56272.1; -  
 DR HSP; P80362; IWTL.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 109  
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C528C7EB197 CRC64;

Query Match  
 Best Local Similarity 66.4%; Score 364.5; DB 4; Length 109;  
 Matches 71; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 2 LTQSPSSVSASVGDVVTITTCRASQGISMTLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60  
 DB 4 MTQSGTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 106  
 QY 61 GSGSGTDTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 106  
 DB 64 GSGSGTDTFTLSTLSLQFEDSATYTCQANSPFYTGQGTVEIKR 109

## RESULT 15

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08VCP0          PRELIMINARY;      PRT;      234 AA.
ID 08VCP0
AC 08VCP0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AA19474.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match      66.3%; Score 364; DB 11; Length 234;
Best Local Similarity 65.1%; Pred. No. 9e-31;
Matches 69; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASYGDRVTITCRASQGISWLAHYOHQPGAKPLIYSASLSQGVSRP 60
DB 23 QLTQSPASLSASVGERVTITCRASENIYSILANYQCKQKSPQLLYNNAKTLDGVPSRP 82
QY 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
DB 83 SSGSRSGTGFSLKINSLOPEDFGSYCCQHSGIGPFTFGSGTKLEIKR 128

```

Search completed: February 10, 2004, 18:39:23  
 Job time : 25.0545 secs

|                       |
|-----------------------|
| Anti-Interleukin-1    |
| Human antibody CAV1   |
| c Human anti-RH-(D)   |
| c Human anti-HER2     |
| TRO005 Humab kappa    |
| Anti-HIV gp120 imm    |
| VL region of HIV      |
| Anti-gp120 antitoo    |
| Anti-gp120 antitoo    |
| Human anti-Rh(D) c    |
| e Human anti-Rh(D) c  |
| Humam KDR (VEGFR-2)   |
| VEGF binding relat    |
| e Human anti-h(D) d   |
| e Insulin/insulin mor |
| HCV EI antigen mol    |
| Human VJ consensu     |
| Consensus human I     |
| Human variable li     |

XX MO200253595-A1.  
 XX 11-JUL-2002.  
 XX 27-DEC-2001; 2001MO-SE02908.  
 XX 29-DEC-2000; 2000SE-0004892.  
 XX (PHAA ) PHARMACIA DIAGNOSTICS AB.  
 XX Flicker S, Steinberger P, Kraft D, Valenta R;  
 XX WPI: 2002-583604/62.  
 XX N-PSDB; ABR9642.  
 XX  
 XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for  
 PT environmental allergen detection -  
 XX  
 XX Disclosure; Page 41; 45pp; English.  
 XX  
 XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's  
 CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).  
 CC The group 2 allergen-specific Fabs of the invention may be useful for  
 CC environmental allergen detection and for standardisation of allergen  
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for  
 CC passive immunotherapy of type I allergy. It is also useful for  
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention  
 CC are useful for inter alia, diagnosis, therapy and prevention of type  
 CC I allergy. They are also useful for identification of group 2  
 CC allergen-containing pollen and may be used for blocking the binding of  
 CC grass pollen allergic patients IgE antibodies to Phi p 2. The present  
 CC sequence represents the human IgG fab, clone 100 light chain protein of  
 CC the invention.  
 XX  
 XX Sequence 106 AA;  
 SQ  
 XX  
 XX Query Match 96.0%; Score 527; DB 23; Length 106;  
 Best Local Similarity 97.2%; Pred. No. 1.4e-30;  
 Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVGVDRVTITCRASQGISWLMAYOHQPKAPKLLIYSASSLSQGVPSRF 60  
 DB 1 ELTQSPSSVSASVGVDRVTITCRASQGISWLMAYOHQPKAPKLLIYSASSLSQGVPSRF 60  
 QY 61 SSGSGYGTDFSLTSSLPEDSATYTYCOQANSFYTFGQGTKEIKR 106  
 DB 61 SSGSGYGTDFSLTSSLPEDSATYTYCOQANSFYTFGQGTKEIKR 106  
 RESULT 2  
 AAB03713  
 ID AAB03713 standard; protein; 233 AA.  
 XX  
 XX AAB03713;  
 XX  
 XX 04-OCT-2000 (first entry)  
 XX  
 XX Immunoglobulin kappa amino acid sequence fragment.  
 XX  
 XX Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;  
 KW abdominal aortic aneurysm disease; treatment; detect; tolerance;  
 KW immunoglobulin kappa, Igk.  
 XX  
 XX Unidentified.  
 OS  
 XX US6048704-A.  
 XX  
 XX

PD 11-APR-2000.  
 XX  
 XX 07-MAR-1997; 97US-0812586.  
 XX  
 XX 07-MAR-1996; 96US-0012976.  
 XX  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 XX Tilson MD;  
 XX  
 XX WPI; 2000-316895/27.  
 XX  
 XX Isolated microfibrillar protein for alleviating abdominal aortic  
 PT aneurysm disease is purified from human aortic tissue and binds  
 PT immunoreactively with immunoglobulin -  
 XX  
 XX Example 3; Column 29-31; 70pp; English.  
 XX  
 XX The present invention relates to an isolated microfibrillar protein of  
 CC approximately 40kD. The protein is isolated from human aortic tissue and  
 CC binds immunoreactively with immunoglobulin purified from human abdominal  
 CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic  
 CC aneurysm-associated antigenic protein (AAP). The protein is capable of  
 CC forming a disulphide bonded dimer. The protein is immunoreactive with  
 CC human kappa immunoglobulin. Also included in the invention are  
 CC recombinantly produced human AAA proteins. AAP shows regions of homology  
 CC with the bovine microfibril associated glycoprotein MFAP-4 and also with  
 CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful  
 CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the  
 CC presence of AAA-associated immunoglobulin bound to the human aortic  
 CC tissue. Antibodies directed against AAP can be used to detect AAA  
 CC disease. The recombinant protein can be used to induce tolerance to  
 CC antigenic AAA protein in the subject e.g. human. This sequence represents  
 CC an immunoglobulin kappa amino acid sequence. The sequence shares homology  
 CC with the AAP of the invention, it was used to identify and characterise  
 CC AAP.  
 XX  
 XX Sequence 233 AA;  
 SQ  
 XX  
 XX Query Match 94.4%; Score 518; DB 21; Length 233;  
 Best Local Similarity 96.2%; Pred. No. 1.2e-29;  
 Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVGVDRVTITCRASQGISWLMAYOHQPKAPKLLIYSASSLSQGVPSRF 60  
 DB 23 ELTQSPSSVSASVGVDRVTITCRASQGISWLMAYOHQPKAPKLLIYSASSLSQGVPSRF 82  
 QY 61 SSGSGYGTDFSLTSSLPEDSATYTYCOQANSFYTFGQGTKEIKR 106  
 DB 83 SSGSGYGTDFSLTSSLPEDSATYTYCOQANSFYTFGQGTKEIKR 128  
 RESULT 3  
 ABB07237  
 ID ABB07237 standard; protein; 107 AA.  
 XX  
 XX ABB07237;  
 XX  
 XX 26-MAR-2002 (first entry)  
 XX  
 XX Anti-IL-4 and IL-13 receptors MAb 63 light chain variable region.  
 XX  
 XX Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;  
 KW antiarthritic; dermatological; antiulcer; antiinflammatory; cytostatic;  
 KW anticlacking; immunosuppressive; tuberculostatic; ophthalmological;  
 KW IL-13; antianemic; antichryd.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH 24..34  
 FT /note="complementarily determining region (CDR) 1"  
 FT Region 50..56  
 FT

| ID                    | ABJ36940  | standard; Protein; 223 AA. |
|-----------------------|---|----------------------------|
| XX                    | ABJ36940;   |                            |
| AC                    | ABJ36940;   |                            |
| DT                    | 01-MAY-2003   | (first entry)              |
| XX                    |   |                            |
| DE                    | Anti-CD40 monoclonal antibody related protein SEQ ID No 66.               |                            |
| XX                    |   |                            |
| KW                    | Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;         |                            |
| KW                    | human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;   |                            |
| KW                    | dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;     |                            |
| KW                    | immunoprecipitor; anti-tumour agent; immunosuppressant; allergy;          |                            |
| KW                    | autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.         |                            |
| OS                    | Unidentified.   |                            |
| XX                    | WO200288186-A1.   |                            |
| XX                    |   |                            |
| PD                    | 07-NOV-2002.  |                            |
| XX                    |   |                            |
| XX                    | 26-APR-2002; 2002WO-JP04292.  |                            |
| XX                    |   |                            |
| PR                    | 27-APR-2001; 2001WO-USJ3672.  |                            |
| PR                    | 11-MAY-2001; 2001JP-0142482.  |                            |
| PR                    | 05-OCT-2001; 2001JP-0310535.  |                            |
| PR                    | 26-OCT-2001; 2001US-0040244.  |                            |
| XX                    |   |                            |
| PA                    | (KIRI ) KIRIN BEER KK.  |                            |
| XX                    |   |                            |
| PI                    | Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;                     |                            |
| DR                    | WPI; 2003-120463/11.  |                            |
| DR                    | N-PSDB; ABT31882.   |                            |
| PT                    | Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,   |                            |
| PT                    | or functional fragment, is useful in the treatment of e.g. autoimmune     |                            |
| PT                    | diseases or cancer  |                            |
| XX                    |   |                            |
| PS                    | Claim 15; Page 60; 94p; Japanese.   |                            |
| XX                    |   |                            |
| CC                    | The invention relates to an antibody to human CD40, or its functional     |                            |
| CC                    | fragment, has at least one of the following properties: acting on         |                            |
| CC                    | dendritic cells to produce IL-12 in the presence of LPS                   |                            |
| CC                    | (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic |                            |
| CC                    | cells to activate maturation of the dendritic cells with high G28-5       |                            |
| CC                    | antibody; and activating CD95 expression with high G28-5 antibody against |                            |
| CC                    | B cell line. Such antibodies or functional fragments can be used as       |                            |
| CC                    | immunoadjuvants, anti-tumour agents, immunosuppressants, and as remedies  |                            |
| CC                    | for autoimmune diseases, allergy or coagulation factor VIII inhibitors    |                            |
| CC                    | syndrome. This sequence represents a protein relating to the anti-CD40    |                            |
| CC                    | monoclonal antibody of the invention.                                     |                            |
| XX                    |   |                            |
| Sequence              | 223 AA;   |                            |
| Query Match           | 88.2%; Score 484; DB 24; Length 223;                                      |                            |
| Best Local Similarity | 87.7%; Pred. No. 3,1e-27;   |                            |
| Matches               | 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;                       |                            |
| QY                    | 1 ELTDSPESSVSAVSDRTTITTCRASQGISSWLAWYQHOPGRKAPKLLIYSASSLSGVSRSR 60        |                            |
| DB                    | 25 QMTDPSPESSVSAVSDRTTITTCRASQGISSWLAWYQHOPGRKAPKLLIYSASSLSGVSRSR 84      |                            |
| QY                    | 61 SGSGYGRDFSLTTSLSLFEDSATYYCOANSPFPTFGQGTVEIKR 106                       |                            |
| DB                    | 85 SGSGYGRDFSLTTSLSLFEDSATYYCOANSPFPTFGQGTVEIKR 130                       |                            |
| RESULT 5              |   |                            |
| AA65571               |   |                            |
| ID                    | AA65571 standard; protein; 107 AA.  |                            |
| XX                    |   |                            |
| CC                    | AA65571;  |                            |

XX 30-NOV-2001 (first entry)  
 XX Amino acid sequence of protein seq Id No. 96.  
 DE Gene library; immunoglobulin; antibody library; human.  
 XX Homo sapiens.  
 OS WO200162907-A1.  
 XX 30-AUG-2001.  
 PD 22-FEB-2001; 2001WO-IP01298.  
 PF 22-FEB-2000; 2000JP-0050543.  
 XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.  
 PA Kurobawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;  
 PI Okuno Y, Shireki K;  
 XX WPI; 2001-565420/63.  
 DR N-PSDB; AAH47735.  
 XX Producing gene libraries and antibody libraries, involves selecting a  
 PT light chain that binds to a heavy chain product to produce a functional  
 PT formation, and producing a gene library of the light chain variable  
 PT regions -  
 XX Examples; p 172; 181pp; Japanese.  
 PS The invention relates to producing gene libraries, comprising  
 CC immunoglobulin light and heavy variable region. The method involves  
 CC selecting light chain that binds with the heavy chain product to produce  
 CC a functional conformation, producing a gene library comprising a  
 CC collection of these light chain variable genes, and combining with gene  
 CC library of heavy chain variable genes. The method is used for production  
 CC of gene and antibody libraries.  
 CC  
 SQ Sequence 107 AA;  
 Query Match 87.1%; Score 478; DB 22; Length 107;  
 Best Local Similarity 88.6%; Pred. No. 4.3e-27; Indels 0; Gaps 0;  
 Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ELTQSSSVASVSGDRVTITCRASOGISWLAHYOHOPGKAPKLLIYSASLSQGVPSRP 60  
 DB 3 QMTQSSSVASVSGDRVTITCRASOGISWLAHYOHOPGKAPKLLIYSASLSQGVPSRP 62  
 QY 61 GSGSGYGFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIK 105  
 DB 63 GSGSGYGFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIK 107  
 RESULT 6  
 ABP45870 ID ABP45870 standard; Protein; 244 AA.  
 XX ABP45870;  
 DT 19-AUG-2002 (first entry)  
 XX Human Bly's binding scFv SEQ ID 1881.  
 DE Human Bly's binding scFv SEQ ID 1881.  
 XX Bly's: B lymphocyte stimulator; TNF superfamily; human; cytosolic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.

XX WO200202641-A1.  
 PN 10-JAN-2002.  
 PD 15-JUN-2001; 2001WO-US91110.  
 PF 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PI WPI; 2002-114799/15.  
 DR Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 PT Claim 1; Page 2646-2647; 3148pp; English.  
 XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
 CC and so may be used to detect and quantitate the presence of BlyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BlyS. They may also be  
 CC administered to treat diseases associated with aberrant BlyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 CC  
 SQ Sequence 244 AA;  
 Query Match 87.1%; Score 478; DB 23; Length 244;  
 Best Local Similarity 88.6%; Pred. No. 9e-27; Indels 0; Gaps 0;  
 Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 LTQSPSSVASVSGDRVTITCRASOGISWLAHYOHOPGKAPKLLIYSASLSQGVPSRP 61  
 DB 140 MTQSPSTLSASVGDRTVITCRASOGISWLAHYOHOPGKAPKLLIYSASLSQGVPSRP 199  
 QY 62 GSGYGFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIK 106  
 DB 200 GSGYGFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIK 244  
 RESULT 7  
 AAU74297 ID AAU74297 standard; Protein; 236 AA.  
 XX AAU74297;  
 DT 12-MAR-2002 (first entry)  
 XX Anti-human Allm monoclonal antibody clone Jmab-136, light chain.  
 DE Anti-human Allm monoclonal antibody clone Jmab-136, light chain.  
 XX Human; antineumatic; antiarthritic; antidiabetic; antipsoriatic;  
 KM immunosuppressive; dermatological; antiinflammatory; hepatotropic;  
 KM immunosuppressive; dermatoecological; antiinflammatory; hepatotropic;  
 KM activation inducible lymphocyte immunomodulatory molecule; Allm;  
 KM monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;  
 OS Homo sapiens.

|  |  |
|--|--|
| OS   | Homo sapiens.  |
| XX   |  |
| PN   | WO200187961-A2.  |
| XX   |  |
| PD   | 22-NOV-2001.   |
| XX   |  |
| PB   | 15-MAY-2001; 2001WO-JP04035.   |
| PF   |  |
| PR   | 18-MAY-2000; 2000JP-0147116.   |
| PR   | 30-MAR-2001; 2001JP-0099508.   |
| PA   | (NISB ) JAPAN TOBACCO INC.   |
| XX   |  |
| PI   | Tsuji T, Tezuka K, Hori N;   |
| XX   |  |
| DR   | WPI; 2002-075313/10.   |
| DR   | N-PSDB; AAS99473.  |
| PT   | New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation -   |
| PT   |  |
| XX   |  |
| PS   | Claim 30; Page 270-271; 300pp; English.  |
| XX   | The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activator-inducible lymphocyte immunomodulatory molecule (AIIIM). (I) is useful for modulating signal transduction into a cell mediated by AIIIM, for modulating proliferation of AIIIM-expressing cells, for modulating production of a cytokine from AIIIM-expressing cells, and for inducing antibody-dependent cytotoxicity against AIIIM-expressing cells and/or immune cytolysis or apoptosis of AIIIM-expressing cells. (I) is useful for treating, preventing or prophylaxis of delayed type allergy. (I) is useful for treating and preventing various diseases associated with AIIIM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the diseases. (I) is useful for suppression, prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic disorders, inflammation, graft versus host reaction, graft versus host disease, immune rejection, disorders caused by abnormal intestinal immunity, specifically inflammatory intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatitis. (I) induces no serious immunorejection due to antigenicity to human, i.e., human anti-mouse antigenicity (HAM) in a host. |
| CC   | AAU74226-AAU74301 represent anti-human AIIIM monoclonal antibody amino acid sequences of the invention.  |
| CC   |  |
| XX   |  |
| SQ   | Sequence 236 AA:   |
|  |  |
| Query Match  | 86.5%; Score 475; DB 23; Length 236;   |
| Best Local Similarity                                      | 88.7%; Pred. No. 1,4e-26;  |
| Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0 |  |
| OY   | 1 ELTSPSSVSASVGRRVTITTCASGISISMLAWOHOPKAPKLITYSASSIQGVPSPRF 60<br>:::     :<br>Db QMTGPSVVSAHSVGRVTTITTCASGISISLWLMMYOKPKAKLLITYVASLIQSGLVSPSRF 84   |
| OY   | 61 SGGSGGTDFSLTISSILQPEDSATYYCQQAENSEPYFGGTKEIKR 106<br>   :   <br>Db 85 SGGSGGTDFTLTISSLQPEDPATYYCQQAENSEPMFTFGQTKEIKR 130<br>   :  |
| RESULT 8   |  |
| ID   | AAO18424 standard; protein; 105 AA.  |

|          |  |
|----------|--|
| XX       | AA018424;  |
| AC       | Best Local Similarity 86.3%; Score 474; DB 23; Length 105;             |
| DT       | Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;            |
| DE       | Anti-GD2 antibody light chain #1.                                      |
| KW       | Anti-GD2 antibody; neuroectodermal tumour; cancer; neuroblastoma;      |
| KM       | melanoma; vaccine; gene therapy; cytostatic; disialoganglioside GD2.   |
| OS       | Homo sapiens.  |
| OS       | Synthetic.   |
| PN       | DE10059930-A1.   |
| PD       | 29-MAY-2002.   |
| PF       | 23-NOV-2000; 2000DE-1059930.   |
| PR       | 23-NOV-2000; 2000DE-1059930.   |
| PA       | (FISC/) FISCHER P.   |
| PA       | (UTTE/) UTTENREUTHER-FISCHER M.  |
| PI       | Uttentreuther-Fischer M, Krueger J;                                    |
| PX       | WPI; 2002-510006/55.   |
| PT       | Composition for treating tumors that produce disialoganglioside GD2,   |
| PT       | comprises human antibody fragment able to induce anti-idiotypic        |
| PS       | antibodies -   |
| PS       | Claim 3; Fig 7A; 14pp; German.   |
| CC       | The present invention relates to a composition for treating tumours    |
| CC       | positive for disialoganglioside GD2 which is based on human antibody   |
| CC       | fragments that activate the immune system against GD2, specifically by |
| CC       | inducing anti-GD2 antibodies. The composition can be used in the       |
| CC       | treatment of neuroblastoma and melanoma. The present sequence is an    |
| CC       | anti-GD2 antibody light chain.   |
| SQ       | Sequence 105 AA;   |
| OY       | Query Match  |
| DB       | 1 ELTQSPSSVSASVGDRVTITTCRASOGISSWLAWYQHOPGKAPKLLIYASSLSQGVPSPRF 60     |
| OY       | 61 SSGSGGTDFSLTISLQPEDSATYYCOOANGFPYPFGGGTKVEIK 105                    |
| DB       | 61 SSGSGGIDFTLTISLQPEDPATYYCOOSYSTPQTFFGGTKVEIK 105                    |
| RESULT 9 |  |
| ID       | AAB72880 standard; Protein; 107 AA.                                    |
| AC       | AAB72880;  |
| DT       | 10-MAY-2001 (first entry)  |
| DE       | Human anti-HER2/neu antibody 3-F2 light chain.                         |
| KW       | Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy;    |
| KM       | 3-F2; 1-D2; 2-E8; growth factor receptor.                              |
| OS       | Homo sapiens.  |
| PN       | WO200109187-A2.  |

PD 08-FEB-2001.  
 XX  
 PF 25-JUL-2000; 2000MO-US20272.  
 XX  
 PR 29-JUL-1999; 99US-0146313.  
 XX  
 PR 10-MAR-2000; 2000US-0188539.  
 XX  
 PA (MEDA-) MEDAREX INC.  
 XX  
 PI Keler T, Deo Y;  
 DR WPI; 2001-168698/17.  
 XX  
 DR N-PSDB; AAF75586.  
 XX  
 PT New human monoclonal antibody that specifically binds to growth factor  
 PT receptor HER2/neu, for treating, preventing or diagnosing diseases  
 PT characterized by aberrant HER2/neu expression e.g. cancers  
 XX  
 PS Disclosure; Page 104-105; 113pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences for human  
 CC monoclonal antibodies which bind specifically to the HER2/neu growth  
 CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2  
 CC and 2-B8. They can be used in the immunotherapy-based treatment and  
 CC prognosis of cancers, particularly adenocarcinomas such as salivary  
 CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,  
 CC and ovarian cancer. The present sequence is part of an antibody of the  
 CC invention.  
 CC  
 SQ Sequence 107 AA;  
 XX  
 QY Query Match 85.1%; Score 467; DB 22; Length 107;  
 Db Best Local Similarity 85.7%; Pred. No. 2.5e-26;  
 Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVGRVITTCRASQGISWLMAYOHQPKAPKLLIYASNSLSQGVPSRF 60  
 Db 3 QMTQSPSSLSASVGRVITTCRASQGISWLMAYQKPEKAPKSLIYASNSLSQGVPSRF 62  
 QY 61 SSGSGYGTDSLTITSSLSQFEDSATYTCQANSFPYTGQGTKEIK 105  
 Db 63 SSGSGGTDFLTITSSLSQPEDFATYTCQVNSPYTFGQGTKEIK 107  
 Db  
 RESULT 10  
 AAUT6522  
 ID AAUT6522 standard; Protein; 108 AA.  
 XX  
 AC AAUT6522;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE Anti-Interleukin-12 (IL-12) antibody variable region #2.  
 XX  
 KW Human; antibody; anti-interleukin-12; CDR; heavy chain; circulatory;  
 KW complementarity determining region; neuroprotective; antiproliferative;  
 KW immunostimulant; cytostatic; anti-microbial; psoriasis; infection;  
 KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;  
 KW neurological disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200212500-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 07-AUG-2001; 2001MO-US24720.  
 XX  
 PR 07-AUG-2000; 2000US-223358P.  
 XX  
 PR 29-SEP-2000; 2000US-236827P.  
 XX  
 PR 01-AUG-2001; 2001US-0920262.  
 XX  
 PA (CENZ) CENTOCOR INC.  
 XX

XX  
 PI Giles-Komar J, Knight DM, Peritt D, Scallion B, Shealy D;  
 XX  
 DR WPI; 2002-257482/30.  
 XX  
 PT New mammalian anti-IL-12 antibodies, useful for diagnosing or treating  
 PT IL-12 related conditions, e.g. psoriasis or multiple sclerosis, as well  
 PT as other for treating immune, infectious, malignant or neurological  
 PT disorders  
 XX  
 PS Claim 1; Page 93-94; 96pp; English.  
 XX  
 CC The invention relates to novel isolated mammalian anti-interleukin-12  
 CC (IL-12) antibodies. The antibodies comprise at least one complementarily  
 CC determining region (CDR) of a heavy or light chain, a heavy chain or  
 CC light chain variable region, or a heavy chain or light chain constant  
 CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or  
 CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.  
 CC The antibodies are also useful for treating immune, cardiovascular,  
 CC infectious, malignant or neurological disorders or diseases. The present  
 CC sequence represents the amino acid sequence of human anti-Interleukin-  
 CC 12 (IL-12) antibody variable region #2.  
 CC  
 SQ Sequence 108 AA;  
 XX  
 QY Query Match 84.9%; Score 466; DB 23; Length 108;  
 Db Best Local Similarity 84.9%; Pred. No. 3.1e-26;  
 Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVGRVITTCRASQGISWLMAYOHQPKAPKLLIYASNSLSQGVPSRF 60  
 Db 3 QMTQSPSSLSASVGRVITTCRASQGISWLMAYQKPEKAPKSLIYASNSLSQGVPSRF 62  
 QY 61 SSGSGYGTDSLTITSSLSQFEDSATYTCQANSFPYTGQGTKEIK 106  
 Db 63 SSGSGGTDFLTITSSLSQPEDFATYTCQVNSPYTFGQGTKEIK 108  
 Db  
 RESULT 11  
 AAEL10815  
 ID AAEL10815 standard; Protein; 109 AA.  
 XX  
 AC AAEL10815;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human antibody CAT-212 light chain variable domain.  
 XX  
 KW Human; eotaxin; CAT-212; antibody; light chain variable region; VL;  
 KW eczema; asthma; atopic disease; dermatological; rhinitis; food allergy;  
 KW vasotropic; conjunctivitis; allergic colitis; psoriasis; pemphigoid;  
 KW eosinophil-mediated disease; cellulitis; drug eruption; vasculitis;  
 KW inflammatory bowel disease; gastroenteritis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..2 /note="Encoded by ACATC"  
 FT  
 XX  
 PN MO200166754-A1.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 02-MAR-2001; 2001MO-GB00927.  
 XX  
 PR 03-MAR-2000; 2000US-187246P.  
 XX  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Vaughan TJ, Wilton AJ, Smith S;  
 XX  
 DR WPI; 2001-589944/66.  
 XX



DR N-PSDB; AAD18149.  
 XX  
 PT Human antibodies against eotaxin useful for treating asthma, eczema and  
 PT other atopic diseases, comprises an antibody variable heavy or variable  
 PT light domain from CAT-212 or from complementary determining regions  
 XX  
 PS Claim 1, Page 102; 107pp; English.  
 CC The invention relates to a specific binding member which binds to human  
 CC eotaxin. The binding member comprises an antibody variable heavy  
 CC (VH)/variable light (VL) domain from CAT-212 VH/VL domain and a VH/VL  
 CC domain comprising one or more VH/VL complementary determining regions  
 CC (CDRs). Eotaxin is a chemottractant protein that binds to a specific  
 CC receptor which is expressed predominantly on eosinophils. The binding  
 CC member is useful for neutralising eotaxin, which is useful in treating  
 CC asthma, eczema and other atopic diseases such as rhinitis, food allergy,  
 CC conjunctivitis, allergic colitis which are recognised as eosinophil-  
 CC mediated diseases; for treating skin and other atopic conditions such as  
 CC psoriasis, pemphigoid, 'wells' syndrome, cellulitis, drug eruptions;  
 CC inflammatory bowel disease which includes eosinophilic colitis/enteritis/  
 CC gastroenteritis/Shulman's syndrome; vasculitis including Hughes-Stovin  
 CC syndrome, Churg-Strazaus syndrome. The present sequence is human  
 CC antibody CAT-212 light chain variable domain (VL) which binds to eotaxin.  
 CC  
 SQ Sequence 109 AA:  
 Query Match 84.6%; Score 464.5; DB 22; Length 109;  
 Best Local Similarity 86.0%; Pred. No. 4e-26;  
 Matches 92; Conservative 8; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 ELTQSPSSVSASVGDRTVTTCRASQGISISMLAWYOHQPKAPKLIIYASSLSQGVPSRF 60  
 DB 3 QNTQSPSSVSASVGDRTVTTCRASQDISISMLAWYQKPKAPKLIIYASSLSQGVPSRF 62  
 QY 61 SSGSGYGTDFSLTISLQFEDSATYTYCCQANSFP-YTFGGGTKEIKR 106  
 DB 63 SSGSGGTDFTLTISLQPEDFATYTCQANSFPSTFFGGTKEIKR 109

RESULT 12  
 AAG93597  
 ID AAG93597 standard; Protein; 107 AA.  
 AC AAG93597;  
 XX  
 DT 14-SEP-2001 (first entry)  
 XX  
 DE Human anti-Rh(D) chain 109 protein sequence.  
 XX  
 DE Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
 KW  
 OS Homo sapiens.  
 XX  
 PN US6255455-B1.  
 PD 03-JUL-2001.  
 PF 29-JAN-1999; 99US-0240274.  
 XX  
 PR 11-OCT-1996; 96US-0028650.  
 PR 10-APR-1998; 98US-0081380.  
 PR 27-JUN-1997; 97US-0884045.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 PI Siegel DL;  
 XX  
 DR WPI; 2001-38931/41.  
 DR N-PSDB; AAG68654.  
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in

PT therapeutic medicine -  
 XX  
 PS Claim 1; Column 44; 162pp; English.  
 XX  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAG68615 to AAG68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification  
 CC of the present invention.  
 CC  
 SQ Sequence 107 AA:  
 Query Match 84.3%; Score 463; DB 22; Length 107;  
 Best Local Similarity 85.8%; Pred. No. 5e-26; Indels 0; Gaps 0;  
 Matches 91; Conservative 7; Mismatches 8;  
 QY 1 ELTQSPSSVSASVGDRTVTTCRASQGISISMLAWYOHQPKAPKLIIYASSLSQGVPSRF 60  
 DB 2 ELTQSPSSVSASVGDRTVTTCRASQGISISMLAWYQKPKAPKLIIYASSLSQGVPSRF 61  
 QY 61 SSGSGYGTDFSLTISLQFEDSATYTYCCQANSFPYTFGGGTKEIKR 106  
 DB 62 SSGSGGTDFTLTISLQPEDFATYTCQANSFPYTFGGGTKEIKR 107

RESULT 13  
 AAB72882  
 ID AAB72882 standard; Protein; 107 AA.  
 AC AAB72882;  
 XX  
 DT 10-MAY-2001 (first entry)  
 XX  
 DE Human anti-HER2/neu antibody 1-D2 light chain.  
 DE  
 DE Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy;  
 KW 3-F2; 1-D2; 2-E8; growth factor receptor.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200109187-A2.  
 PD 08-FEB-2001.  
 PF 25-JUL-2000; 2000WO-US20272.  
 XX  
 PR 29-JUL-1999; 99US-0146313.  
 PR 10-MAR-2000; 2000US-0188539.  
 XX  
 PA (MEDA-) MEDAREX INC.  
 PI Keller T; Deo Y;  
 XX  
 DR WPI; 2001-168698/17.  
 DR N-PSDB; AAF75588.  
 PT New human monoclonal antibody that specifically binds to growth factor  
 PT receptor HER2/neu, for treating, preventing or diagnosing diseases  
 PT characterized by aberrant HER2/neu expression e.g. cancers -  
 XX  
 PS Disclosure; Page 107; 113pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences for human  
 CC monoclonal antibodies which bind specifically to the HER2/neu growth  
 CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2  
 CC and 2-E8. They can be used in the immunotherapy-based treatment and  
 CC prognosis of cancers, particularly adenocarcinomas such as salivary

CC dicistronic vector to produce a 11

Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification using primers specific for heavy and light chain variable regions. The amplification products were inserted into a distronic vector to produce a library of fragments. E.coli XL1 blue cells were transformed with the library. Filamentous phage were

CC produced which expressed the MAb regions on their surface. Panning  
 CC with gp120 and gp41 resulted in the recovery of immunoreactive  
 CC clones. The light chain VK region sequence AAR54260 neutralises HIV1  
 CC gp120.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 107 AA;

Query Match 83.8%; Score 460; DB 15; Length 107;  
 Best Local Similarity 85.8%; Pred. No. 8.2e-26;  
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTSPSSVSASVGDRTTTCRASQGISMLAWYOHOPKAPKLIYSASSLSQGVPSRF 60  
 DB 1 ELTSPSSLSASVGDRTTTCRASQGISMLAWYOHOPKAPKLIYSASSLSQGVPSRF 60  
 QY 61 SSGSGYTDFTLTISSLSQFEDSATYCCQANSPFPTFGGKTKEIKR 106  
 DB 61 SSGSGYTDFTLTISSLSQFEDSATYCCQANSPFPTFGGKTKEIKR 106

Search completed: February 10, 2004, 18:36:12  
 Job time : 32.9606 secs

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; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-159
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```

Query Match      87.8%; Score 482; DB 12; Length 107;
Best Local Similarity 88.6%; Pred. No. 4e-36;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPKAPKLLIYSASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYQOKPKAPKLLIYAASLSQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SSGSGYTDPSLTITSLQPEDSATYTCQANSFPYTGQGTKEIK 105
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGTDFTLTITSLQPEDFATYTCQANSFPITFGQGTREIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

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RESULT 3
US-10-309-762-62
; Sequence 62, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-62
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```

Query Match      87.2%; Score 479; DB 12; Length 107;
Best Local Similarity 88.6%; Pred. No. 7.4e-36;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPKAPKLLIYSASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYQOKPKAPKLLIYAASLSQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SSGSGYTDPSLTITSLQPEDSATYTCQANSFPYTGQGTKEIK 105
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGTDFTLTITSLQPEDFATYTCQANSFPITFGQGTREIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 4
US-10-309-762-164
; Sequence 164, Application US/10309762
; Publication No. US20040018198A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-164
```

```

Query Match      87.2%; Score 479; DB 12; Length 107;
Best Local Similarity 88.6%; Pred. No. 7.4e-36;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPKAPKLLIYSASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYQOKPKAPKLLIYAASLSQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SSGSGYTDPSLTITSLQPEDSATYTCQANSFPYTGQGTKEIK 105
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGTDFTLTITSLQPEDFATYTCQANSFPITFGQGTREIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 5
US-10-309-762-61
; Sequence 61, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-61
```

```

Query Match      87.1%; Score 478; DB 12; Length 107;
Best Local Similarity 87.6%; Pred. No. 9.1e-36;
Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPKAPKLLIYSASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYQOKPKAPKLLIYAASLSQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SSGSGYTDPSLTITSLQPEDSATYTCQANSFPYTGQGTKEIK 105
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGTDFTLTITSLQPEDFATYTCQANSFPITFGQGTREIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 6
US-10-309-762-64
; Sequence 64, Application US/10309762
```

Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gaillo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN  
FILE REFERENCE: ABGENIX-027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 64  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-64

Query Match 87.1%; Score 478; DB 12; Length 107;  
Best Local Similarity 87.6%; Pred. No. 9,1e-36;  
Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSVSVGDRVTITTCRASQGISWLAHYQHGRKAPKLLIYASASSLQSGVPSRF 60  
DB 3 QMTQSPSSVSVSVGDRVTITTCRASQGISWLAHYQHGRKAPKLLIYASASSLQSGVPSRF 62  
QY 61 SGGSGTDFSLTITSLQPEDSATYCCOANSFPYFGGKTVEIKR 105  
DB 63 SGGSGTDFSLTITSLQPEDPATYCCOANSFPITFGGKTVEIKR 107

RESULT 7  
US-09-880-748-1881  
Sequence 1881, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1881  
LENGTH: 244  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-1881

Query Match 87.1%; Score 478; DB 11; Length 244;  
Best Local Similarity 88.6%; Pred. No. 2,1e-35;  
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 LTQSSSVSVSVGDRVTITTCRASQGISWLAHYQHGRKAPKLLIYASASSLQSGVPSRF 61  
DB 140 MTQSSSVSVSVGDRVTITTCRASQGISWLAHYQHGRKAPKLLIYASASSLQSGVPSRF 199  
QY 62 GSGYGTDFSLTITSLQPEDSATYCCOANSFPYFGGKTVEIKR 106  
DB 200 GSGGTDFSLTITSLQPEDPATYCCOANSFPITFGGKTVEIKR 244

RESULT 8  
US-09-859-053-30  
Sequence 30, Application US/09859053  
Patent No. US20020102658A1  
GENERAL INFORMATION:  
APPLICANT: Tezuka, Takashi  
APPLICANT: Hori, No. US20020102658A1  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLM AND  
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
FILE REFERENCE: 06501-079001  
CURRENT APPLICATION NUMBER: US/09/859,053  
CURRENT FILING DATE: 2001-05-16  
PRIOR APPLICATION NUMBER: JP 2001-99508  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: JP 2000-147116  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 236  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-859-053-30

Query Match 86.5%; Score 475; DB 10; Length 236;  
Best Local Similarity 88.7%; Pred. No. 3,7e-35;  
Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSVSVGDRVTITTCRASQGISWLAHYQHGRKAPKLLIYASASSLQSGVPSRF 60  
DB 25 QMTQSPSSVSVSVGDRVTITTCRASQGISWLAHYQHGRKAPKLLIYASASSLQSGVPSRF 84  
QY 61 SGGSGTDFSLTITSLQPEDSATYCCOANSFPYFGGKTVEIKR 106  
DB 85 SGGSGTDFSLTITSLQPEDPATYCCOANSFPITFGGKTVEIKR 130

RESULT 9  
US-10-041-860-43  
Sequence 43, Application US/10041860  
Publication No. US20030157109A1  
GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.  
APPLICANT: Jia, Xiao-Chi  
APPLICANT: Feng, Xiao  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Chen, Francine  
APPLICANT: Gazit, Gadi  
APPLICANT: Weber, Richard  
APPLICANT: Bezabeh, Binyam  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: ABGENIX-051A  
CURRENT APPLICATION NUMBER: US/10/041,860  
CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 43  
LENGTH: 107  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-43

Query Match 86.3%; Score 474; DB 12; Length 107;  
Best Local Similarity 87.6%; Pred. No. 2,1e-35;  
Matches 92; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSVSVGDRVTITTCRASQGISWLAHYQHGRKAPKLLIYASASSLQSGVPSRF 60  
DB 140 MTQSSSVSVSVGDRVTITTCRASQGISWLAHYQHGRKAPKLLIYASASSLQSGVPSRF 199

Db 3 QMTQSSSVASVAGDVRTTTCRASQGISWLAHYQOKPKAKPLLIYAASLQSGVPSRF 62  
QY 61 SSGSGYTDPSLTITSSLOFEDSATYCCOQANSFPYTGQGTKEIK 105  
Db 63 SSGSGGTDFTLTITSSLOPEDFASYCCOQNSFPRTGQGTKEIK 107

## RESULT 10

US-10-041-860-218  
; Sequence 218, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gad  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Biniam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES  
; FILE REFERENCE: ABGENIX.051A  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: US/10/041,860  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 218  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-218

Query Match 86.3%; Score 474; DB 12; Length 107;  
Best Local Similarity 87.6%; Pred. No. 2.1e-35;  
Matches 92; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVRTTTCRASQGISWLAHYQOKPKAKPLLIYAASLQSGVPSRF 60  
Db 3 QMTQSSSVASVAGDVRTTTCRASQGISWLAHYQOKPKAKPLLIYAASLQSGVPSRF 62  
QY 61 SSGSGYTDPSLTITSSLOFEDSATYCCOQANSFPYTGQGTKEIK 105  
Db 63 SSGSGGTDFTLTITSSLOPEDFASYCCOQNSFPRTGQGTKEIK 107

## RESULT 11

US-10-309-762-84  
; Sequence 84, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudae, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: US/10/309,762  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-84

Query Match 86.2%; Score 473.5; DB 12; Length 106;  
Best Local Similarity 89.5%; Pred. No. 2.3e-35;  
Matches 94; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSVASVAGDVRTTTCRASQGISWLAHYQOKPKAKPLLIYAASLQSGVPSRF 60  
Db 3 QMTQSSSVASVAGDVRTTTCRASQGISWLAHYQOKPKAKPLLIYAASLQSGVPSRF 62  
QY 61 SSGSGYTDPSLTITSSLOFEDSATYCCOQANSFPYTGQGTKEIK 105  
Db 63 SSGSGGTDFTLTITSSLOPEDFASYCCOQNSFPRTGQGTKEIK 106

## RESULT 12

US-10-309-762-60  
; Sequence 60, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudae, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: US/10/309,762  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 60  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-60

Query Match 86.0%; Score 472; DB 12; Length 107;  
Best Local Similarity 86.7%; Pred. No. 3.1e-35;  
Matches 91; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVRTTTCRASQGISWLAHYQOKPKAKPLLIYAASLQSGVPSRF 60  
Db 3 QMTQSSSVASVAGDVRTTTCRASQGISWLAHYQOKPKAKPLLIYAASLQSGVPSRF 62  
QY 61 SSGSGYTDPSLTITSSLOFEDSATYCCOQANSFPYTGQGTKEIK 105  
Db 63 SSGSGGTDFTLTITSSLOPEDFASYCCOQNSFPRTGQGTKEIK 107

## RESULT 13

US-10-309-762-63  
; Sequence 63, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudae, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: US/10/309,762  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-63

Query Match 86.0%; Score 472; DB 12; Length 107;  
Best Local Similarity 86.7%; Pred. No. 3.1e-35;





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